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The invention relates to methods to select breeding animals or animals destined for slaughter for having desired genotypic or potential phenotypic properties, in particular related to muscle mass and/or fat deposition. Breeding schemes for domestic animals have so far focused on farm performance traits and carcass quality. This has resulted in substantial improvements in traits like reproductive success, milk production, lean/fat ratio, prolificacy, growth rate and feed efficiency. Relatively simple performance test data have been the basis for these improvements, and selected traits were assumed to be influenced by a large number of genes, each of small effect (the infinitesimal gene model). There are now some important changes occurring in this area. First, the breeding goal of some breeding organisations has begun to include meat quality attributes in addition to the "traditional" production traits. Secondly, evidence is accumulating that current and new breeding goal traits may involve relatively large effects (known as major genes), as opposed to the infinitesimal model that has been relied on so far.

Modern DNA-technologies provide the opportunity to exploit these major genes, and this approach is a very promising route for the improvement of meat quality, especially since direct meat quality assessment is not viable for potential breeding animals. Also for other traits such as lean/fat ratio, growth rate and feed efficiency, modern DNA technology can be very effective. Also these traits are not always easy to measure in the living animal.

The evidence for several of the major genes originally obtained using segregation analysis, i.e. without any DNA marker information. Afterwards molecular studies were performed to detect the location of these

genes on the genetic map. In practice, and except for alleles of very large effect, DNA studies are required to dissect the genetic nature of most traits of economic importance. DNA markers can be used to localise genes or alleles responsible for qualitative traits like coat colour, and they can also be used to detect genes or alleles with substantial effects on quantitative traits like growth rate, IMF etc. In this case the approach is referred to as QTL (quantitative trait locus) mapping, wherein a QTL comprises at least a part of the nucleic acid genome of an animal where genetic information capable of influencing said quantitative trait (in said animal or in its offspring) is located. Information at DNA level can not only help to fix a specific major gene in a population, but also assist in the selection of a quantitative trait which is already selected for. Molecular information in addition to phenotypic data can increase the accuracy of selection and therefore the selection response.

Improving meat quality or carcass quality is not just about changing levels of traits like tenderness or marbling, but it is also about increasing uniformity. The existence of major genes provides excellent opportunities for improving meat quality because it allows large steps to be made in the desired direction. Secondly, it will help to reduce variation, since we can fix relevant genes in our products. Another aspect is that selecting for major genes allows differentiation for specific markets. Studies are underway in several species, particularly, pigs, sheep, deer and beef cattle.

In particular, intense selection for meat production has resulted in animals with extreme muscularity and leanness in several livestock species. In recent years it has become feasible to map and clone several of the genes causing these phenotypes, paving the way towards more efficient marker assisted selection, targeted drug development (performance enhancing products) and transgenesis. Mutations in the ryanodine receptor (Fuji

et al, 1991; MacLennan and Phillips, 1993) and myostatin (Grobet et al, 1997; Kambadur et al, 1997; McPherron and Lee, 1997) have been shown to cause muscular hypertrophies in pigs and cattle respectively, while
5 genes with major effects on muscularity and/or fat deposition have for instance been mapped to pig chromosome 4 (Andersson et al, 1994) and sheep chromosome 18 (Cocket et al, 1996).

However, although there have been successes in
10 identifying QTLs, the information is currently of limited use within commercial breeding programmes. Many workers in this field conclude that it is necessary to identify the particular genes underlying the QTL. This is a substantial task, as the QTL region is usually relatively
15 large and may contain many genes. Identification of the relevant genes from the many that may be involved thus remains a significant hurdle in farm animals.

The invention provides a method for selecting a
20 domestic animal for having desired genotypic or potential phenotypic properties comprising testing said animal for the presence of a parentally imprinted qualitative or quantitative trait locus (QTL). Herein, a domestic animal is defined as an animal being selected or having been
25 derived from an animal having been selected for having desired genotypic or potential phenotypic properties.

Domestic animals provide a rich resource of genetic and phenotypic variation, traditionally domestication involves selecting an animal or its offspring for having
30 desired genotypic or potential phenotypic properties. This selection process has in the past century been facilitated by growing understanding and utilisation of the laws of Mendelian inheritance. One of the major problems in breeding programs of domestic animals is the
35 negative genetic correlation between reproductive capacity and production traits. This is for example the case in cattle (a high milk production generally results

in slim cows and bulls) poultry, broiler lines have a low level of egg production and layers have generally very low muscle growth), pigs (very prolific sows are in general fat and have comparatively less meat) or sheep (high prolific breeds have low carcass quality and vice versa). The invention now provides that knowledge of the parental imprinting character of various traits allows to select for example sire lines homozygous for a paternally imprinted QTL for example linked with muscle production or growth; the selection for such traits can thus be less stringent in dam lines in favour of the reproductive quality. The phenomenon of genetic or parental imprinting has never been utilised in selecting domestic animals, it was never considered feasible to employ this elusive genetic characteristic in practical breeding programmes. The invention provides a breeding programme, wherein knowledge of the parental imprinting character of a desired trait, as demonstrated herein, results in a breeding programme, for example in a BLUP programme, with a modified animal model. This increases the accuracy of the breeding value estimation and speeds up selection compared to conventional breeding programmes. Until now, the effect of a parentally imprinted trait in the estimation of a conventional BLUP programme was neglected; using and understanding the parental character of the desired trait, as provided by the invention, allows selecting on parental imprinting, even without DNA testing. For example, selecting genes characterised by paternal imprinting is provided to help increase uniformity; a (terminal) parent homozygous for the "good or wanted" alleles will pass them to all offspring, regardless of the other parent's alleles, and the offspring will all express the desired parent's alleles. This results in more uniform offspring. Alleles that are interesting or favourable from the maternal side or often the ones that have opposite effects to alleles from the paternal side. For example, in meat animals such as pigs alleles linked with meat quality traits such as intra-

muscular fat or muscle mass could be fixed in the dam lines while alleles linked with reduced back fat could be fixed in the sire lines. Other desirable combinations are for example fertility and/or milk yield in the female line with growth rates and/or muscle mass in the male lines.

In a preferred embodiment, the invention provides a method for selecting a domestic animal for having desired genotypic or potential phenotypic properties comprising testing a nucleic acid sample from said animal for the presence of a parentally imprinted quantitative trait locus (QTL). A nucleic acid sample can in general be obtained from various parts of the animal's body by methods known in the art. Traditional samples for the purpose of nucleic acid testing are blood samples or skin or mucosal surface samples, but samples from other tissues can be used as well, in particular sperm samples, oocyte or embryo samples can be used. In such a sample, the presence and/or sequence of a specific nucleic acid, be it DNA or RNA, can be determined with methods known in the art, such as hybridisation or nucleic acid amplification or sequencing techniques known in the art. The invention provides testing such a sample for the presence of nucleic acid wherein a QTL or allele associated therewith is associated with the phenomenon of parental imprinting, for example where it is determined whether a paternal or maternal allele of said QTL is capable of being predominantly expressed in said animal.

The purpose of breeding programs in livestock is to enhance the performances of animals by improving their genetic composition. In essence this improvement accrues by increasing the frequency of the most favourable alleles for the genes influencing the performance characteristics of interest. These genes are referred to as QTL. Until the beginning of the nineties, genetic improvement was achieved via the use of biometrical methods, but without molecular knowledge of the underlying QTL.

Since the beginning of the nineties and due to recent developments in genomics, it is conceivable to identify the QTL underlying a trait of interest. The invention now provides identifying and using parentally imprinted QTLs which are useful for selecting animals by mapping quantitative trait loci. Again, the phenomenon of genetic or paternal imprinting has never been utilised in selecting domestic animals, it was never considered feasible to employ this elusive genetic characteristic in practical breeding programmes. For example Kovacs and Kloting (Biochem. Mol. Biol. Int. 44:399-405, 1998), where parental imprinting is not mentioned, and not suggested, found linkage of a trait in female rats, but not in males, suggesting a possible sex specificity associated with a chromosomal region, which of course excludes parental imprinting, a phenomenon wherein the imprinted trait of one parent is preferably but gender-aspecifically expressed in his or her offspring.

The invention provides the initial localisation of a parentally imprinted QTL on the genome by linkage analysis with genetic markers, and the actual identification of the parentally imprinted gene(s) and causal mutations therein. Molecular knowledge of such a parentally imprinted QTL allows for more efficient breeding designs herewith provided. Applications of molecular knowledge of parentally imprinted QTLs in breeding programs include: marker assisted segregation analysis to identify the segregation of functionally distinct parentally imprinted QTL alleles in the populations of interest, marker assisted selection (MAS) performed within lines to enhance genetic response by increasing selection accuracy, selection intensity or by reducing the generation interval using the understanding of the phenomenon of parental imprinting, marker assisted introgression (MAI) to efficiently transfer favourable parentally imprinted QTL alleles from a donor to a recipient population, genetic engineering of the identified parentally QTL and genetic modification of the breeding stock using transgenic technology, development

of performance enhancing products using targeted drug development exploiting molecular knowledge of said QTL.

The inventors undertook two independent experiments to determine the practical use of parental imprinting of

5 a QTL.

In a first experiment, performed in a previously described Piétrain x Large White intercross, the likelihood of the data were computed under a model of paternal (paternal allele only expressed) and maternal
10 imprinting (maternal allele only expressed) and compared with the likelihood of the data under a model of a conventional "Mendelian" QTL. The results strikingly demonstrated that the QTL was indeed paternally expressed, the QTL allele (Piétrain or Large White)
15 inherited from the F₁ sow having no effect whatsoever on the carcass quality and quantity of the F₂ offspring. It was seen that very significant lodscores were obtained when testing for the presence of a paternally expressed QTL, while there was no evidence at all for the
20 segregation of a QTL when studying the chromosomes transmitted by the sows. The same tendency was observed for all traits showing that the same imprinted gene is responsible for the effects observed on the different traits. Table 1 reports the maximum likelihood (ML)
25 phenotypic means for the F₂ offspring sorted by inherited paternal QTL allele.

In a second experiment performed in the Wild Boar X Large White intercross, QTL analyses of body composition, fatness, meat quality, and growth traits was carried out
30 with the chromosome 2 map using a statistical model testing for the presence of an imprinting effect. Clear evidence for a paternally expressed QTL located at the very distal tip of 2p was obtained (Fig. 2; Table1). The clear paternal expression of a QTL is illustrated by the
35 least squares means which fall into two classes following the population origin of the paternally inherited allele (Table 1). For a given paternally imprinted QTL, implementation of marker assisted segregation analysis, selection (MAS) and introgression (MAI), can be performed

using genetic markers that are linked to the QTL, genetic markers that are in linkage disequilibrium with the QTL, or using the actual causal mutations within the QTL.

Understanding the parent-of-origin effect

5 characterising a QTL allows for its optimal use in breeding programs. Indeed, marker assisted segregation analysis under a model of parental imprinting will yield better estimates of QTL allele effects. Moreover it allows for the application of specific breeding schemes
10 to optimally exploit a QTL. In one embodiment of the invention, the most favourable QTL alleles would be fixed in breeding animal lines and for example used to generate commercial, crossbred males by marker assisted selection (MAS, within lines) and marker assisted introgression
15 (MAI, between lines). In another embodiment, the worst QTL alleles would be fixed in the animal lines used to generate commercial crossbred females by MAS (within lines) and MAI (between lines).

In a preferred embodiment of the invention, said
20 animal is a pig. Note for example that the invention provides the insight that today half of the offspring from commercially popular Piétrain, Large White crossbred boars inherit an unfavourable Large White muscle mass QTL as provided by the invention causing considerable loss,
25 and the invention now for example provides the possibility to select the better half of the population in that respect. However, it is also possible to select commercial sow lines enriched with the in the boars unfavourable alleles, allowing to equip the sows with
30 other alleles more desirable for for example reproductive purposes.

In a preferred embodiment of a method provided by the invention, said QTL is located at a position corresponding to a QTL located at chromosome 2 in the
35 pig. For example, it is known from comparative mapping data between pig and human, including bidirectional chromosome painting, that SSC2p is homologous to HSA11pter-q13^{11,12}. HSA11pter-q13 is known to harbour a

cluster of imprinted genes: IGF2, INS2, H19, MAH2, P57^{KIP2}, K_LQTL1, Tapal/CD81, Orct12, Impt1 and Ip1. The cluster of imprinted genes located in HSA11pter-q13 is characterised by 8 maternally expressed genes H19, MASH2, P57^{KIP2}, K_LQTL1, TAPAL/CD81, ORCTL2, IMPT1 and IP1, and two paternally expressed genes: IGF2 and INS. However, Johanson et al (Genomics 25:682-690, 1995) and Reik et al (Trends in Genetics, 13:330-334, 1997) show that the whereabouts of these loci in various animals are not clear. For example, the HSA11 and MMU7 loci do not correspond among each other, the MMU7 and the SSC2 loci do not correspond, whereas the HSA11 and SSC2 loci seem to correspond, and no guidance is given where one or more of for example the above identified parentally expressed individual genes are localised on the three species' chromosomes.

Other domestic animals, such as cattle, sheep, poultry and fish, having similar regions in their genome harbouring such a cluster of imprinted genes or QTLs, the invention herewith provides use of these orthologous regions of other domestic animals in applying the phenomenon of parental imprinting in breeding programmes. In pigs, said cluster is mapped at around position 2p1.7 of chromosome 2, however, a method as provided by the invention employing (fragments of) said maternally or paternally expressed orthologous or homologous genes or QTLs are advantageously used in other animals as well for breeding and selecting purposes. For example, a method is provided wherein said QTL is related to the potential muscle mass and/or fat deposition, preferably with limited effects on other traits such as meat quality and daily gain of said animal or wherein said QTL comprises at least a part of an insulin-like growth factor-2 (IGF2) allele. Reik et al (Trends in Genetics, 13:330-334, 1997) explain that this gene in humans is related to Beckwith-Wiedemann syndrome, an apparently parentally imprinted disease syndrome most commonly seen with human foetuses, where the gene has an important role in prenatal

development. No relationship is shown or suggested with postnatal development relating to muscle development or fatness in (domestic) animals.

In a preferred embodiment, the invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7. In particular, the invention relates to the use of genetic markers for the telomeric end of pig chromosome 2p in marker selection (MAS) of a parentally imprinted Quantitative Trait Locus (QTL) affecting carcass yield and quality in pigs. Furthermore, the invention relates to the use of genetic markers associated with the IGF2 locus in MAS in pigs, such as polymorphisms and microsatellites and other characterising nucleic acid sequences shown herein, such as shown in figures 4 to 10. In a preferred embodiment, the invention provides a QTL located at the distal tip of *Sus scrofa* chromosomes 2 with effects on various measurements of carcass quality and quantity, particularly muscle mass and fat deposition.

In a first experiment, a QTL mapping analysis was performed in a Wild Boar X Large White intercross counting 200 F₂ individuals. The F₂ animals were sacrificed at a live weight of at least 80 kg or at a maximum age of 190 days. Phenotypic data on birth weight, growth, fat deposition, body composition, weight of internal organs, and meat quality were collected; a detailed description of the phenotypic traits are provided by Andersson et al¹ and Andersson-Eklund et al⁴.

A QTL (without any significant effect on back-fat thickness) at an unspecified locus on the proximal end of chromosome 2 with moderate effect on muscle mass, and located about 30cM away from the parentally imprinted QTL reported here, was previously reported by the inventors; whereas the QTL as now provided has a very large effect, explaining at least 20-30% of variance, making the QTL of

the present invention commercially very attractive, which is even more so because the present QTL is parentally imprinted. The marker map of chromosome 2p was improved as part of this invention by adding microsatellite markers in order to cover the entire chromosome arm. The following microsatellite markers were used: *Swc9*, *Sw2443*, *Sw2623*, and *Swr2516*, all from the distal end of 2p⁷. QTL analyses of body composition, fatness, meat quality, and growth traits were carried out with the new chromosome 2 map. Clear evidence for a QTL located at the very distal tip of 2p was obtained (Fig. 1; Table 1). The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F₂ population. Large effects on the area of the longissimus dorsi muscle, on the weight of the heart, and on back-fat thickness (subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population.

In a second experiment, QTL mapping was performed in a Piétrain X Large White intercross comprising 1125 F₂ offspring. The Large White and Piétrain parental breeds differ for a number of economically important phenotypes. Piétrains are famous for their exceptional muscularity and leanness¹⁰ (Figure 2, while Large Whites show superior growth performance. Twenty-one distinct phenotypes measuring growth performance (5), muscularity (6), fat deposition (6), and meat quality (4), were recorded on all F₂ offspring. In order to map QTL underlying the genetic differences between these breeds, the inventors undertook a whole genome scan using microsatellite markers on an initial sample of 677 F₂ individuals. The following microsatellite marker map was used to analyse

- chromosome 2; SW2443, SWC9 and SW2623, SWR2516-(0,20)-SWR783-(0,29)-SW240-(0,20)-SW776-(0,08)-S0010-(0,04)-SW1695-(0,36)-SWR308. Analysis of pig chromosome 2 using a Maximum Likelihood multipoint algorithm, revealed
- 5 highly significant lodscores (up to 20) for three of the six phenotypes measuring muscularity (% lean cuts, % ham, % loin) and three of the six phenotypes measuring fat deposition (back-fat thickness (BFT), % backfat, % fat cuts) at the distal end of the short arm of chromosome 2
- 10 (Figure 1). Positive lodscores were obtained in the corresponding chromosome region for the remaining six muscularity and fatness phenotypes, however, not reaching the experiment-wise significance threshold ($\alpha=5\%$). There was no evidence for an effect of the corresponding QTL on
- 15 growth performance (including birth weight) or recorded meat quality measurements (data not shown). To confirm this finding, the remaining sample of 355 F₂ offspring was genotyped for the four most distal 2p markers and QTL analysis performed for the traits yielding the highest
- 20 lodscores in the first analysis. Lodscores ranged from 2.1 to 7.7, clearly confirming the presence of a major QTL in this region. Table 2 reports the corresponding ML estimates for the three genotypic means as well as the residual variance. Evidence based on marker assisted
- 25 segregation analysis points towards residual segregation at this locus within the Piétrain population.
- These experiments therefore clearly indicated the existence of a QTL with major effect on carcass quality and quantity on the telomeric end of pig
- 30 chromosome arm 2p; the likely existence of an allelic series at this QTL with at least three alleles: Wild-Boar < Large White < Piétrain, and possibly more given the observed segregation within the Piétrain breed.
- The effects of the identified QTL on muscle mass and
- 35 fat deposition are truly major, being of the same magnitude of those reported for the *CRC* locus though apparently without the associated deleterious effects on meat quality. We estimate that both loci jointly explain

close to 50% of the Piétrain versus Large White breed difference for muscularity and leanness. The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F_2 population. Large effects on the area of the longissimus dorsi muscle, on the weight of the heart, and on back-fat thickness (subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL, when compared to the Wild Boar allele, was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population. The strong imprinting effect observed for all affected traits shows that a single causative locus is involved. The pleiotropic effects on skeletal muscle mass and the size of the heart appear adaptive from a physiological point of view as a larger muscle mass requires a larger cardiac output.

In a further embodiment, the invention provides a method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7., wherein said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele or a genomic area closely related thereto, such as polymorphisms and microsatellites and other characterising nucleic acid sequences shown herein, such as shown in figures 4 to 10. The important role of *IGF2* for prenatal development is well-documented from knock-out mice as well as from its causative role in the human Beckwith-Wiedemann syndrome. This invention demonstrates an important role for the *IGF2*-region also for postnatal development.

To show the role of *Igf2* the inventors performed the following three experiments:

A genomic *IGF2* clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone
5 gave a strong consistent signal on the terminal part of chromosome 2p.

A polymorphic microsatellite is located in the 3'UTR of *IGF2* in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible
10 presence of a corresponding porcine microsatellite was investigated by direct sequencing of the *IFG2* 3'UTR using the BAC clone. A complex microsatellite was identified about 800bp downstream of the stop codon; a sequence comparison revealed that this microsatellite was
15 identical to a previously described anonymous microsatellite, *Swc9*⁶. This marker was used in the initial QTL mapping experiments and its location on the genetic map correspond with the most likely position of the QTL both in the Piétrain X Large White and in the Large White
20 x Wild Boar pedigree.

Analysis of skeletal muscle and liver cDNA from 10-week old fetuses heterozygous for a nt241 (G-A) transversion in the second exon of the porcine *IGFII* gene and *SWC9*, shows that the *IGFII* gene is imprinted in these
25 tissues in the pig as well and only expressed from the paternal allele.

Based on a published porcine adult liver cDNA sequence¹⁶, the inventors designed primer pairs allowing to amplify the entire *IgfII* coding sequence with 222 bp
30 of leader and 280 bp of trailer sequence from adult skeletal muscle cDNA. Piétrain and Large White RT-PCR products were sequenced indication that the coding sequences are identical in both breeds and with the published sequence. However, a G→A transition was found
35 in the leader sequence corresponding to exon 2 in man. Following conventional nomenclature, this polymorphism will be referred to as nt241(G-A). We developed a screening test for this single nucleotide polymorphism

9(SNP) based on the ligation amplification reaction (LAR), allowing us to genotype our pedigree material. Based on these data, *Igf1I* was shown to colocalize with the SWC9 microsatellite marker ($\theta=0\%$), therefore

5 virtually coinciding with the most likely position of the QTL, and well within the 95% support interval for the QTL. Subsequent sequence analysis demonstrated that the microsatellite marker SWC9 is actually located within the 3'UTR of the *Igf1I* gene.

10 As previously mentioned, the knowledge of this QTL provides a method for the selection of animals such as pigs with improved carcass merit. Different embodiments of the invention are envisaged, including: marker assisted segregation analysis to identify the
15 segregation of functionally distinct QTL alleles in the populations of interest; marker assisted selection (MAS) performed within lines to enhance genetic response by increasing selection accuracy, selection intensity or by reducing the generation interval; marker assisted
20 introgression (MAI) to efficiently transfer favourable QTL alleles from a donor to a recipient population, thereby enhancing genetic response in the recipient population. Implementation of embodiments marker assisted segregation analysis, selection (MAS) and introgression
25 (MAI), can be performed using genetic markers that are linked to the QTL; genetic markers that are in linkage disequilibrium with the QTL, the actual causal mutations within the QTL.

In a further embodiment, the invention provides a
30 method for selecting a pig for having desired genotypic or potential phenotypic properties comprising testing a sample from said pig for the presence of a quantitative trait locus (QTL) located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7., wherein said QTL is
35 paternally expressed, i.e. is expressed from the paternal allele. In man and mouse, *Igf2* is known to be imprinted and to be expressed exclusively from the paternal allele in several tissues. Analysis of skeletal muscle cDNA from

pigs heterozygous for the SNP and/or SWC9, shows that the same imprinting holds in the pig as well. Understanding the parent-of-origin effect characterising the QTL as provided by the invention now allows for its optimal use in breeding programs. Indeed, today half of the offspring from commercially popular Piétrain x Large White crossbred boars inherit the unfavourable Large White allele causing considerable loss. Using a method as provide by the invention avoids this problem.

10 The invention furthermore provides an isolated and/or recombinant nucleic acid or functional fragment derived thereof comprising a parentally imprinted quantitative trait locus (QTL) or fragment thereof capable of being predominantly expressed by one parental
15 allele. Having such a nucleic acid as provided by the invention available allows constructing transgenic animals wherein favourable genes are capable of being exclusively or predominantly expressed by one parental allele, thereby equipping the offspring of said animal
20 homozygous for a desired trait with desired properties related to that parental allele that is expressed.

In a preferred embodiment, the invention provides an isolated and/or recombinant nucleic acid or fragment derived thereof comprising a synthetic parentally
25 imprinted quantitative trait locus (QTL) or functional fragment thereof derived from at least one chromosome. Synthetic herein describes a parentally expressed QTL wherein various elements are combined that originate from distinct locations from the genome of one or more
30 animals. The invention provides recombinant nucleic acid wherein sequences related to parental imprinting of one QTL are combined with sequences relating to genes or favourable alleles of a second QTL. Such a gene construct is favourably used to obtain transgenic animals wherein
35 the second QTL has been equipped with paternal imprinting, as opposed to the inheritance pattern in the native animal from which the second QTL is derived. Such a second QTL can for example be derived from the same

chromosome where the parental imprinting region is located, but can also be derived from a different chromosome from the same or even a different species. In the pig, such a second QTL can for example be related to an oestrogen receptor (ESR)-gene (Rothschild et al, PNAS, 93, 201-201, 1996) or a FAT-QTL (Andersson, Science, 263, 1771-1774, 1994) for example derived from an other pig chromosome, such as chromosome 4. A second or further QTL can also be derived from another (domestic) animal or a human.

The invention furthermore provides an isolated and/or recombinant nucleic acid or functional fragment derived thereof at least partly corresponding to a QTL of a pig located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7 wherein said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or wherein said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele, preferably at least spanning a region between INS and H19, or preferably derived from a domestic pig, such as a Pietrain, Meishan, Duroc, Landrace or Large White, or from a Wild Boar. For example, a genomic IGF2 clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone gave a strong consistent signal on the terminal part of chromosome 2p. A polymorphic microsatellite is located in the 3'UTR of IGF2 in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible presence of a corresponding porcine microsatellite was investigated by direct sequencing of the IGF2 3'UTR using the BAC clone. A complex microsatellite was identified about 800 bp downstream of the stop codon; a sequence comparison revealed that this microsatellite is identical to a previously described anonymous microsatellite, Swc9. PCR primers were designed and the microsatellite (IGF2ms) was found to be highly polymorphic with three different alleles among the two Wild Boar founders and another two

among the eight Large White founders. *IGF2ms* was fully informative in the intercross as the breed of origin as well as the parent of origin could be determined with confidence for each allele in each F_2 animal.

5 A linkage analysis using the intercross pedigree was carried out with *IGF2ms* and the microsatellites *Sw2443*, *Sw2623*, and *Swr2516*, all from the distal end of 2p⁷. *IGF2* was firmly assigned to 2p by highly significant lod scores (e.g. $Z=89.0$, $\theta=0.003$ against *Swr2516*). Multipoint
10 analyses, including previously typed chromosome 2 markers, revealed the following order of loci (sex-average map distances in Kosambi cM): *Sw2443/Swr2516*-0.3-*IGF2*-14.9-*Sw2623*-10.3-*Sw256*. No recombinant was observed between *Sw2443* and *Swr2516*, and the suggested proximal
15 location of *IGF2* in relation to these loci is based on a single recombinant giving a lod score support of 0.8 for the reported order. The most distal marker in our previous QTL study, *Sw256*, is located about 25 cM from the distal end of the linkage group.

20 The invention furthermore provides use of a nucleic acid or functional fragment derived thereof according to the invention in a method according to the invention. In a preferred embodiment, use of a method according to invention is provided to select a breeding animal or
25 animal destined for slaughter, or embryos or semen derived from these animals for having desired genotypic or potential phenotypic properties. In particular, the invention provides such use wherein said properties are related to muscle mass and/or fat deposition. The QTL as
30 provided by the invention may be exploited or used to improve for example lean meat content or back-fat thickness by marker assisted selection within populations or by marker assisted introgression of favorable alleles from one population to another. Examples of marker
35 assisted selection using the QTL as provided by the invention are use of marker assisted segregation analysis

with linked markers or with markers in disequilibrium to identify functionally distinct QTL alleles. Furthermore, identification of a causative mutation in the QTL is now possible, again leading to identify functionally distinct QTL alleles. Such functionally distinct QTL alleles located at the distal tip of chromosome 2p with large effects on skeletal muscle mass, the size of the heart, and on back-fat thickness are also provided by the invention. The observation of a similar QTL effect in a Large White x Wild Boar as well as in a Piétrain x Large White intercross provides proof of the existence of a series of at least three distinct functional alleles. Moreover, preliminary evidence based on marker assisted segregation analysis points towards residual segregation at this locus within the Piétrain population (data not shown). The occurrence of an allelic series as provided by the invention allows identifying causal polymorphisms which - based on the quantitative nature of the observed effect - are unlikely to be gross gene alterations but rather subtle regulatory mutations. The effects on muscle mass of the three alleles rank in the same order as the breeds in which they are found i.e. Piétrain pigs are more muscular than Large White pigs that in turn have higher lean meat content than Wild Boars. The invention furthermore provides use of the alleles as provided by the invention for within line selection or for marker assisted introgression using linked markers, markers in disequilibrium or alleles comprising causative mutations.

The invention furthermore provides an animal selected by using a method according to the invention. For example, a pig characterised in being homozygous for an allele in a QTL located at a *Sus scrofa* chromosome 2 mapping at position 2p1.7 can now be selected and is thus provided by the invention. Since said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or said QTL comprises at least a part of a *Sus scrofa* insulin-like growth factor-2 (IGF2) allele, it is

possible to select promising pigs to be used for breeding or to be slaughtered. In particular an animal according to the invention which is a male is provided. Such a male, or its sperm or an embryo derived thereof can advantageously be used in breeding animals for creating breeding lines or for finally breeding animals destined for slaughter. In a preferred embodiment of such use as provided by the invention, a male, or its sperm, deliberately selected for being homozygous for an allele causing the extreme muscular hypertrophy and leanness, is used to produce offspring heterozygous for such an allele. Due to said allele's paternal expression, said offspring will also show the favourable traits for example related to muscle mass, even if the parent female has a different genetic background. Moreover, it is now possible to positively select the female(s) for having different traits, for example related to fertility, without having a negative effect on the muscle mass trait that is inherited from the allele from the selected male. For example, earlier such males could occasionally be seen with Piétrain pigs but genetically it was not understood how to most profitably use these traits in breeding programmes.

Furthermore, the invention provides a transgenic animal, sperm and an embryo derived thereof, comprising a synthetic parentally imprinted QTL or functional fragment thereof as provided by the invention, i.e. it is provided by the invention to introduce a favourable recombinant allele; for example introduce the oestrogen receptor locus related to increased litter size of an animal homozygously in a parentally imprinted region of a grandparent animal (for example the father of a hybrid sow if the region was paternally imprinted and the grandparent was a boar); to introduce a favourable fat-related allele or muscle mass-related recombinant allele in a paternally imprinted region, and so on. Recombinant alleles that are interesting or favourable from the maternal side or often the ones that have opposite effects to alleles from the paternal side. For example,

in meat animals such as pigs recombinant alleles linked with meat quality traits such as intra-muscular fat or muscle mass could be fixed in the dam lines while recombinant alleles linked with reduced back fat could be fixed in the sire lines. Other desirable combinations are for example fertility and/or milk yield in the female line with growth rates and/or muscle mass in the male lines.

The invention is further explained in the detailed description without limiting the invention.

Detailed description.

Example 1: Wild Boar x Large White intercrosses

Methods

Isolation of an *IGF2* BAC clone and fluorescent *in situ* hybridization (FISH). *IGF2* primers (F:5'-GGCAAGTTCTTCCGCTAATGA-3' and R:5'-GCACCGCAGAATTACGACAA-3') for PCR amplification of a part of the last exon and 3'UTR were designed on the basis of a porcine *IGF2* cDNA sequence (GenBank X56094). The primers were used to screen a porcine BAC library and the clone 253G10 was isolated. Crude BAC DNA was prepared as described²⁴. The BAC DNA was linearized with *EcoRV* and purified with QIAEXII (QIAGEN GmbH, Germany). The clone was labeled with biotin-14-dATP using the GIBCO-BRL Bionick labeling system (BRL18246-015). Porcine metaphase chromosomes were obtained from pokeweed (Seromed) stimulated lymphocytes using standard techniques. The slides were aged for two days at room temperature and then kept at -20°C until use. FISH analysis was carried out as previously described²⁵. The final concentration of the probe in the hybridization mix was 10 ng/μl. Repetitive sequences were suppressed with standard concentrations of porcine

genomic DNA. After post-hybridization washing, the biotinylated probe was detected with two layers of avidin-FITC (Vector A-2011). The chromosomes were counterstained with 0.3 mg/ml DAPI (4,6-Diamino-2-phenylindole; Sigma D9542), which produced a G-banding like pattern. No posthybridization banding was needed, since chromosome 2 is easily recognized without banding. A total of 20 metaphase spreads were examined under an Olympus BX-60 fluorescence microscope connected to an IMAC-CCD S30 video camera and equipped with an ISIS 1.65 (Metasystems) software.

Sequence, microsatellite, and linkage analysis.

About two µg of linearized and purified BAC DNA was used for direct sequencing with 20 pmoles of primers and BigDye Terminator chemistry (Perkin Elmer, USA). DNA sequencing was done from the 3' end of the last exon towards the 3' end of the UTR until a microsatellite was detected. A primer set (F:5'-GTTTCTCCTGTACCCACACGCATCCC-3' and R:5'-Fluorescein-CTACAAGCTGGGCTCAGGG-3') was designed for the amplification of the IGF2 microsatellite which is about 250 bp long and located approximately 800 bp downstream from the stop codon. The microsatellite was PCR amplified using fluorescently labeled primers and the genotyping was carried out using an ABI377 sequencer and the GeneScan/Genotyper softwares (Perkin Elmer, USA). Two-point and multipoint linkage analysis were done with the Cri-Map software²⁶.

Animals and phenotypic data.

The intercross pedigree comprised two European Wild Boar males and eight Large White females, 4 F₁ males and 22 F₁ females, and 200 F₂ progeny¹. The F₂ animals were sacrificed at a live weight of at least 80 kg or at a

maximum age of 190 days. Phenotypic data on birth weight, growth, fat deposition, body composition, weight of internal organs, and meat quality were collected; a detailed description of the phenotypic traits are provided by Andersson et al.¹ and Andersson-Eklund et al.⁴

Statistical analysis.

Interval mapping for the presence of QTL were carried out with a least squares method developed for the analysis of crosses between outbred lines²⁷. The method is based on the assumption that the two divergent lines are fixed for alternative QTL alleles. There are four possible genotypes in the F₂ generation as regards the grandparental origin of the alleles at each locus. This makes it possible to fit three effects: additive, dominance, and imprinting². The latter is estimated as the difference between the two types of heterozygotes, the one receiving the Wild Boar allele through an F₁ sire and the one receiving it from an F₁ dam. An F-ratio was calculated using this model (with 3 d.f.) versus a reduced model without a QTL effect for each cM of chromosome 2. The most likely position of a QTL was obtained as the location giving the highest F-ratio. Genome-wise significance thresholds were obtained empirically by a permutation test²⁸ as described². The QTL model including an imprinting effect was compared with a model without imprinting (with 1 d.f.) to test whether the imprinting effect was significant.

The statistical models also included the fixed effects and covariates that were relevant for the respective traits; see Andersson-Eklund et al.⁴ for a more detailed description of the statistical models used. Family was included to account for background genetic

effects and maternal effects. Carcass weight was included as a covariate to discern QTL effects on correlated traits, which means that all results concerning body composition were compared at equal weights. Least-squares means for each genotype class at the *IGF2* locus were estimated with a single point analysis using Procedure GLM of SAS²⁹; the model included the same fixed effects and covariates as used in the interval mapping analyses. The QTL shows a clear parent of origin-specific expression and the map position coincides with that of the insulin-like growth factor II gene (*IGF2*), indicating *IGF2* as the causative gene. A highly significant segregation distortion (excess of Wild Boar-derived alleles) was also observed at this locus. The results demonstrate an important effect of the *IGF2* region on postnatal development and it is possible that the presence of a paternally expressed *IGF2*-linked QTL in humans and in rodent model organisms has so far been overlooked due to experimental design or statistical treatment of data. The study has also important implications for quantitative genetics theory and practical pig breeding.

IGF2 was identified as a positional candidate gene for this QTL due to the observed similarity between pig chromosome 2p and human chromosome 11p. A genomic *IGF2* clone was isolated by screening a porcine BAC library. FISH analysis with this BAC clone gave a strong consistent signal on the terminal part of chromosome 2p (Fig. 1). A polymorphic microsatellite is located in the 3'UTR of *IGF2* in mice (GenBank U71085), humans (GenBank S62623), and horse (GenBank AF020598). The possible presence of a corresponding porcine microsatellite was investigated by direct sequencing of the *IGF2* 3'UTR using the BAC clone. A complex microsatellite was identified about 800 bp downstream of the stop codon; a sequence comparison revealed that this microsatellite is identical

- to a previously described anonymous microsatellite, *Swc96*. PCR primers were designed and the microsatellite (*IGF2ms*) was found to be highly polymorphic with three different alleles among the two Wild Boar founders and another two among the eight Large White founders. *IGF2ms* was fully informative in the intercross as the breed of origin as well as the parent of origin could be determined with confidence for each allele in each F_2 animal.
- 10 A linkage analysis using the intercross pedigree was carried out with *IGF2ms* and the microsatellites *Sw2443*, *Sw2623*, and *Swr2516*, all from the distal end of 2p⁷. *IGF2* was firmly assigned to 2p by highly significant lod scores (e.g. $Z=89.0$, $\theta=0.003$ against *Swr2516*). Multipoint
- 15 analyses, including previously typed chromosome 2 markers⁸, revealed the following order of loci (sex-average map distances in Kosambi cM): *Sw2443/Swr2516*-0.3-*IGF2*-14.9-*Sw2623*-10.3-*Sw256*. No recombinant was observed between *Sw2443* and *Swr2516*, and the suggested proximal
- 20 location of *IGF2* in relation to these loci is based on a single recombinant giving a lod score support of 0.8 for the reported order. The most distal marker in our previous QTL study, *Sw256*, is located about 25 cM from the distal end of the linkage group.
- 25 QTL analyses of body composition, fatness, meat quality, and growth traits were carried out with the new chromosome 2 map using a statistical model testing for the possible presence of an imprinting effect as expected for *IGF2*. Clear evidence for a paternally expressed QTL
- 30 located at the very distal tip of 2p was obtained (Fig. 2; Table 1). The QTL had very large effects on lean meat content in ham and explained an astonishing 30% of the residual phenotypic variance in the F_2 population. Large effects on the area of the longissimus dorsi muscle, on
- 35 the weight of the heart, and on back-fat thickness

(subcutaneous fat) were also noted. A moderate effect on one meat quality trait, reflectance value, was indicated. The QTL had no significant effect on abdominal fat, birth weight, growth, weight of liver, kidney, or spleen (data not shown). The Large White allele at this QTL was associated with larger muscle mass and reduced back-fat thickness consistent with the difference between this breed and the Wild Boar population. The strong imprinting effect observed for all affected traits strongly suggests a single causative locus. The pleiotropic effects on skeletal muscle mass and the size of the heart appear adaptive from a physiological point of view as a larger muscle mass requires a larger cardiac output. The clear paternal expression of this QTL is illustrated by the least squares means which fall into two classes following the population origin of the paternally inherited allele (Table 1). It is worth noticing though that there was a non-significant trend towards less extreme values for the two heterozygous classes, in particular for the estimated effect on the area of longissimus dorsi. This may be due to chance, but could have a biological explanation, e.g. that there is some expression of the maternally inherited allele or that there is a linked, non-imprinted QTL with minor effects on the traits in question.

The *IGF2*-linked QTL and the *FAT1* QTL on chromosome 4, 9 are by far the two loci with the largest effect on body composition and fatness segregating in this Wild Boar intercross. The *IGF2* QTL controls primarily muscle mass whereas *FAT1* has major effects on fat deposition including abdominal fat, a trait that was not affected by the *IGF2* QTL (Fig. 2). No significant interaction between the two loci was indicated and they control a very large proportion of the residual phenotypic variance in the F_2 generation. A model including both QTLs explains 33.1% of the variance for percentage lean meat in ham, 31.3% for the percentage of lean meat plus bone in back, and 26.2%

for average back fat depth (compare with a model including only chromosome 2 effects, Table 1). The two QTLs must have played a major role in the response during selection for lean growth and muscle mass in the Large White domestic pig.

A highly significant segregation distortion was observed in the *IGF2* region (excess of Wild Boar-derived alleles) as shown in Table 1 ($\chi^2=11.7$, d.f.=2; $P=0.003$). The frequency of Wild Boar-derived *IGF2* alleles was 59% in contrast to the expected 50% and there was twice as many "Wild Boar" as "Large White" homozygotes. This deviation was observed with all three loci at the distal tip and is thus not due to typing errors. The effect was also observed with other loci but the degree of distortion decreased as a function of the distance to the distal tip of the chromosome. Blood samples for DNA preparation were collected at 12 weeks of age and we are convinced that the deviation from expected Mendelian ratios was present at birth as the number of animals lost prior to blood sampling was not sufficient to cause a deviation of this magnitude. No other of the more than 250 loci analyzed in this pedigree show such a marked segregation distortion (L. Andersson, unpublished). The segregation distortion did not show an imprinting effect, as the frequencies of the two reciprocal types of heterozygotes were identical (Table 1). This does not exclude the possibility that the QTL effects and the segregation distortion are controlled by the same locus. The segregation distortion maybe due to meiotic drive favoring the paternally expressed allele during gametogenesis, as the F_1 parents were all sired by Wild Boar males. Another possibility is that the segregation distortion may be due to codominant expression of the maternal and paternal allele in some tissues and/or during a critical period of embryo development. Biallelic *IGF2* expression has been reported to occur to some extent

during human development^{10, 11} and interestingly a strong influence of the parental species background on *IGF2* expression was recently found in a cross between *Mus musculus* and *Mus spretus*¹². It is also interesting that a VNTR polymorphism at the insulin gene, which is very closely linked to *IGF2*, is associated with size at birth in humans¹³. It is possible that the *IGF2*-linked QTL in pigs has a minor effect on birth weight but in our data it was far from significant (Fig. 2) and there was no indication of an imprinting effect.

This study is an advance in the general knowledge concerning the biological importance of the *IGF2* locus. The important role of *IGF2* for prenatal development is well-documented from knock-out mice¹⁴ as well as from its causative role in the human Beckwith-Wiedemann syndrome¹⁵. This study demonstrates an important role for the *IGF2*-region also for postnatal development. It should be stressed that our intercross between outbred populations is particularly powerful to detect QTL with a parent of origin-specific effect on a multifactorial trait. This is because multiple alleles (or haplotypes) are segregating and we could deduce whether a heterozygous F_2 animal received the Wild Boar allele from the F_1 male or female. It is quite possible that the segregation of a paternally expressed *IGF2*-linked QTL affecting a trait like obesity has been overlooked in human studies or in intercrosses between inbred rodent populations because of experimental design or statistical treatment of data. An imprinting effect cannot be detected in an intercross between two inbred lines as only two alleles are segregating at each locus. Our result has therefore significant bearings on the future analysis of the association between genetic polymorphism in the *insulin-IGF2* region and Type I diabetes¹⁶, obesity¹⁷, and variation in birth weight¹³ in humans, as

well as for the genetic dissection of complex traits using inbred rodent models. A major impetus for generating an intercross between the domestic pig and its wild ancestor was to explore the possibilities to map and identify major loci that have responded to selection. We have now showed that two single QTLs on chromosome 2 (this study) and 4¹, 2 explain as much as one third of the phenotypic variance for lean meat content in the F₂ generation. This is a gross deviation from the underlying assumption in the classical infinitesimal model in quantitative genetics theory namely that quantitative traits are controlled by an infinite number of loci each with an infinitesimal effect. If a large proportion of the genetic difference between two divergent populations (e.g. Wild Boar and Large White) is controlled by a few loci, one would assume that selection would quickly fix QTL alleles with large effects leading to a selection plateau. However, this is not the experience in animal breeding programs or selection experiments where good persistent long-term selection responses are generally obtained, provided that the effective population size is reasonably large¹⁸. A possible explanation for this paradox is that QTL alleles controlling a large proportion of genetic differences between two populations may be due to several consecutive mutations; this may be mutations in the same gene or at several closely linked genes affecting the same trait. It has been argued that new mutations contribute substantially to long-term selection responses¹⁹, but the genomic distribution of such mutations are unknown.

The search for a single causative mutation is the paradigm as regards the analysis of genetic defects in mice and monogenic disorders in humans. We propose that this may not be the case for loci that have been under selection for a large number of generations in domestic animals, crops, or natural populations. This hypothesis

predicts the presence of multiple alleles at major QTL. It gains some support from our recent characterization of porcine coat color variation. We have found that both the alleles for dominant white color and for black-spotting
5 differ from the corresponding wild-type alleles by at least two consecutive mutations with phenotypic effects at the *KIT* and *MC1R* loci, respectively^{20, 21}. In this context it is highly interesting that in the accompanying example we have identified a third allele at the *IGF2*-
10 linked QTL. The effects on muscle mass of the three alleles rank in the same order as the breeds in which they are found i.e. Piétrain pigs are more muscular than Large White pigs that in turn have higher lean meat content than Wild Boars.

15 There are good reasons to decide that *IGF2* is the causative gene for the now reported QTL. Firstly, there is a perfect agreement in map localization (Fig. 2). Secondly, it has been shown that *IGF2* is paternally expressed in mice, humans, and now in pigs, like the QTL.
20 There are several other imprinted genes in the near vicinity of *IGF2* in mice and humans (*Mash2*, *INS2*, *H19*, *KVLQT1*, *TAPA1/CD81*, and *CDKN1C/p57^{KIP2}*) but only *IGF2* is paternally expressed in adult tissues²². We believe that this locus provides a unique opportunity for molecular
25 characterization of a QTL. The clear paternal expression can be used to exclude genes that do not show this mode of inheritance. Moreover, the presence of an allelic series should facilitate the difficult distinction between causative mutations and linked neutral
30 polymorphism. We have already shown that there is no difference in coding sequence between *IGF2* alleles from Piétrain and Large White pigs suggesting that the causative mutations occur in regulatory sequences. An obvious step is to sequence the entire *IGF2* gene and its
35 multiple promoters from the three populations. The recent

report that a VNTR polymorphism in the promoter region of the insulin (*INS*) gene affects *IGF2* expression²³ suggests that the causative mutations may be at a considerable distance from the *IGF2* coding sequence.

- 5 The results have several important implications for the pig breeding industry. They show that genetic imprinting is not an esoteric academic question but need to be considered in practical breeding programs. The detection of three different alleles in Wild Boar, Large
- 10 White, and Piétrain populations indicates that further alleles at the *IGF2*-linked QTL segregate within commercial populations. The paternal expression of the QTL facilitates its detection using large paternal half-sib families as the female contribution can be ignored.
- 15 The QTL is exploited to improve lean meat content by marker assisted selection within populations or by marker assisted introgression of favorable alleles from one population to another.
-

Example 2: Piétrain x Large White intercrosses

Methods

Pedigree material: The pedigree material utilized to map

- 5 QTL was selected from a previously described Piétrain x Large White F2 pedigree comprising > 1,800 individuals^{6,7}. To assemble this F2 material, 27 Piétrain boars were mated to 20 Large White sows to generate an F1 generation comprising 456 individuals. 31 F1 boars were mated to
10 unrelated 82 F1 sows from 1984 to 1989, yielding a total of 1862 F2 offspring. F1 boars were mated on average to 7 females, and F1 sows to an average of 2,7 males. Average offspring per boar were 60 and per sow 23.

- 15 *Phenotypic information:* (i) *Data collection:* A total of 21 distinct phenotypes were recorded in the F2 generation^{6,7}. These included:
- five growth traits: birth weight (g), weaning weight (Kg), grower weight (Kg), finisher weight (Kg) and
20 average daily gain (ADG; Kg/day; grower to finisher period);
 - two body proportion measurements: carcass length (cm); and a conformation score (0 to 10 scale; ref.6);
 - ten measurements of carcass composition obtained by
25 dissection of the chilled carcasses 24 hours after slaughter. These include measurements of muscularity: % ham (weight hams/carcass weight), % loin (weight loin/carcass weight), % shoulder (weight
30 shoulder/carcass weight), % lean cuts (% ham + %loin + % shoulder); and measurements of fatness: average back-fat thickness (BFT; cm), % backfat (weight backfat/carcass weight), % belly (weight belly/carcass weight), % leaf fat (weight leaf fat/carcass weight), % jowl (weight jowl/carcass weight), and "% fat cuts" (% backfat + %
35 belly + % leaf fat + % jowl).
 - four meat quality measurements: pH _{LD1} (*Longissimus dorsi* 1

hour after slaughter), pH _{LD24} (*Longissimus dorsi* 24 hours after slaughter), pH _{G1} (*Gracilis* 1 hour after slaughter) and pH _{G24} (*Gracilis* 24 hours after slaughter). (ii) *Data processing*: Individual phenotypes were preadjusted for fixed effects (sire, dam, CRC genotype, sex, year-season, parity) and covariates (litter size, birth weight, weaning weight, grower weight, finisher weight) that proved to significantly affect the corresponding trait. Variables included in the model were selected by stepwise regression.

10

Marker genotyping: Primer pairs utilized for PCR amplification of microsatellite markers are as described¹⁹. Marker genotyping was performed as previously described²⁰. Genotypes at the *CRC* and *MyoD* loci were determined using conventional methods as described^{1,12}. The LAR test for the *Igf2* SNP was developed according to Baron et al.²¹ using a primer pair for PCR amplification (5'-CCCCCTGAAGTGGAGGACGAGCAGCC-3'; 5'-ATCGCTGTGGGCTGGGTGGGCTGCC-3') and a set of three primers for the LAR step (5'-FAM-CGCCCCAGCTGCCCCCAG-3'; 5'-HEX-CGCCCCAGCTGCCCCCAA-3'; 5'-CCTGAGCTGCAGCAGGCCAG-3').

20

Map construction: Marker maps were constructed using the TWOPOINT, BUILD and CHROMPIC options of the CRIMAP package²².

25

To allow utilisation of this package, full-sib families related via the boar or sow were disconnected and treated independently. By doing so, some potentially usable information was neglected, yielding, however, unbiased estimates of recombination rates.

30

QTL mapping: (i) *Mapping Mendelian QTL*: Conventional QTL mapping was performed using a multipoint maximum likelihood method. The applied model assumed one segregating QTL per

chromosome, and fixation of alternate QTL alleles in the respective parental lines, Piétrain (P) and Large White (LW). A specific analysis program had to be developed to account for the missing genotypes of the parental generation, resulting in the fact that the parental origin of the F1 chromosomes could not be determined. Using a typical "interval mapping" strategy, an hypothetical QTL was moved along the marker map using user-defined steps. At each position, the likelihood (L) of the pedigree data was computed as:

$$L = \sum_{g=1}^r \prod_{i=1}^n \sum_{G=1}^4 (P(G|M_i, \theta, \phi) P(y_i|G))$$

P or right chromosome P), there is a total of 2^r combinations for r F1 parents.

$$\prod_{i=1}^n n \text{ F2}$$

$\sum_{G=1}^4$ ith F2 offspring, over the four possible QTL genotypes:

P/P, P/LW, LW/P and LW/LW

$P(G|M_i, \theta, \phi)$: the marker genotype of the i th F2 offspring and its F1 parents, (ii) : the vector of recombination rates between adjacent markers and between the hypothetical QTL and its flanking markers, and (iii) θ the considered marker-QTL phase combination of the F1 parents.

Recombination rates and marker linkage phase of F1 parents are assumed to be known when computing this probability. Both were determined using CRIMAP in the map construction phase (see above).

$P(y_i|G) y_i$) of offspring i , given the QTL genotype under consideration. This probability is computed from the normal density function:

$$P(y_i|G) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(y_i - \mu_g)^2}{2\sigma^2}}$$

μ_g is the phenotypic mean of the considered QTL genotype (PP, PL, LP or LL) and σ^2 the residual variance σ^2 was considered to be the same for the four QTL genotypic classes.

- 5 The values of μ_{PP} , $\mu_{PL}=\mu_{LP}$, μ_{LL} and σ^2 maximizing L were determined using the GEMINI optimisation routine²³. The likelihood obtained under this alternative H_1 hypothesis was compared with the likelihood obtained under the null hypothesis H_0 of no QTL, in which the phenotypic means of the
- 10 four QTL genotypic classes were forced to be identical. The difference between the logarithms of the corresponding likelihoods yields a lodscore measuring the evidence in favour of a QTL at the corresponding map position.

- (ii) *Significance thresholds*: Following Lander & Botstein²⁴,
- 15 lodscore thresholds (T) associated with a chosen genome-wide significance level, were computed such that:

$$\alpha = (C + 9.21GT) \chi_1^2(4.6T)$$

C corresponds to the number of chromosomes (= 19), G corresponds to the length of the genome in Morgans (= 29),

- 20 and $\chi_1^2(4.6T)$ denotes one minus the cumulative distribution function of the chi-squared distribution with 2 d.f. Single point $2\ln(LR)$ were assumed to be distributed as a chi-squared distribution with two degrees of freedom, as we were fitting both an additive and dominance component. To account for the
- 25 fact that we were analysing multiple traits, significance levels were adjusted by applying a Bonferoni correction corresponding to the effective number of independent traits that were analyzed. This effective number was estimated at 16 following the approach described by Spelman et al.²⁵.
- 30 Altogether, this allowed us to set the lodscore threshold associated with an experiment-wise significance level of 5%

at 5.8. When attempting to confirm the identified QTL in an independent sample, the same approach was used, however, setting C at 1, G at 25cM and correcting for the analysis of 4.5 independent traits (as only six traits were analyzed in this sample). This yielded a lodscore threshold associated with a Type I error of 5% of 2.

(iii). *Testing for an imprinted QTL*: To test for an imprinted QTL, we assumed that only the QTL alleles transmitted by the parent of a given sex would have an effect on phenotype, the QTL alleles transmitted by the other parent being "neutral". The likelihood of the pedigree data under this hypothesis was computed using equation 1. To compute $P(y_i | G)$, however, the phenotypic means of the four QTL genotypes were set at $\mu_{PP} = \mu_{PL} = \mu_P$ and $\mu_{LP} = \mu_{LL} = \mu_L$ to test for a QTL for which the paternal allele only is expressed, and $\mu_{PP} = \mu_{LP} = \mu_P$ and $\mu_{PL} = \mu_{LL} = \mu_L$ to test for a QTL for which the maternal allele only is expressed. It is assumed in this notation that the first subscript refers to the paternal allele, the second subscript to the maternal allele. H_0 was defined as the null-hypothesis of no QTL, H_1 testing the presence of a Mendelian QTL; H_2 testing the presence of a paternally expressed QTL, and H_3 testing the presence of a maternally expressed QTL.

RT-PCR: Total RNA was extracted from skeletal muscle according to Chirgwin et al.²⁶. RT-PCR was performed using the Gene-Amp RNA PCR Kit (Perkin-Elmer). The PCR products were purified using QiaQuick PCR Purification kit (Qiagen) and sequenced using Dye terminator Cycle Sequencing Ready Reaction (Perkin Elmer) and an ABI373 automatic sequencer.

In example 2 we report the identification of a QTL with major effect on muscle mass and fat deposition mapping to porcine 2p1.7. The QTL shows clear evidence for parental imprinting strongly suggesting the involvement of the *Igf2* locus.

5 A Piétrain X Large White intercross comprising 1125 F₂ offspring was generated as described^{6,7}. The Large White and Piétrain parental breeds differ for a number of economically important phenotypes. Piétrains are famed for their exceptional muscularity and leanness⁸ (Figure 2), while Large
10 Whites show superior growth performance. Twenty-one distinct phenotypes measuring (i) growth performance (5), (ii) muscularity (6), (iii) fat deposition (6), and (iv) meat quality (4), were recorded on all F₂ offspring.

 In order to map QTL underlying the genetic differences
15 between these breeds, we undertook a whole genome scan using microsatellite markers on an initial sample of 677 F₂ individuals. Analysis of pig chromosome 2 using a ML multipoint algorithm, revealed highly significant lodscores (up to 20) for six of the 12 phenotypes measuring muscularity
20 and fat deposition at the distal end of the short arm of chromosome 2 (Figure 3a). Positive lodscores were obtained for the remaining six phenotypes, however, not reaching the genome-wise significance threshold ($\alpha = 5\%$). To confirm this finding, the remaining sample of 355 F₂ offspring was
25 genotyped for the five most distal 2p markers and QTL analysis performed for the traits yielding the highest lodscores in the first analysis. Lodscores ranged from 2.1 to 7.7, clearly confirming the presence of a major QTL in this region. Table 2 reports the corresponding ML estimates for
30 the three genotypic means as well as the corresponding residual variance.

 Bidirectional chromosome painting establishes a correspondence between SSC2p and HSA11pter-q13^{9,10}. At least

two serious candidate genes map to this region in man: the myogenic basic helix-loop-helix factor, *MyoD*, maps to HSA11p15.4, while *Igf2* maps to HSA11p15.5. *MyoD* is a well known key regulator of myogenesis and is one of the first myogenic markers to be switched on during development¹¹. A previously described amplified sequence polymorphism in the porcine *MyoD* gene¹² proved to segregate in our F₂ material, which was entirely genotyped for this marker. Linkage analysis positioned the *MyoD* gene in the SW240-SW776 (odds > 1000) interval, therefore well outside the lod-2 drop off support interval for the QTL (figure 1). *Igf2* is known to enhance both proliferation and differentiation of myoblasts *in vitro*¹³ and to cause a muscular hypertrophy when overexpressed *in vivo*. Based on a published porcine adult liver cDNA sequence¹⁴, we designed primer pairs allowing us to amplify the entire *Igf2* coding sequence with 222 bp of leader and 280 bp of trailer sequence from adult skeletal muscle cDNA. Piétrain and Large White RT-PCR products were sequenced indicating that the coding sequences was identical in both breeds and with the published sequence. However, a G A transition was found in the leader sequence corresponding to exon 2 in man (Figure 4). We developed a screening test for this single nucleotide polymorphism (SNP) based on the ligation amplification reaction (LAR), allowing us to genotype our pedigree material. Based on these data, *Igf2* was shown to colocalize with the SWC9 microsatellite marker (= 0%), therefore located at approximately 2 centimorgan from the most likely position of the QTL and well within the 95% support interval for the QTL (figure 1). Subsequent sequence analysis demonstrated that the microsatellite marker SWC9 is actually located within the 3' UTR of the *Igf2* gene. Combined with available comparative mapping data for the PGA and FSH loci, these results suggest the occurrence of an interstitial

inversion of a chromosome segment containing *MyoD*, but not *Igf2* which has remained telomeric in both species.

Igf2 therefore appeared as a strong positional allele having the observed QTL effect. In man and mouse, *Igf2* is known to be imprinted and to be expressed exclusively from the paternal allele in several tissues¹⁵. Analysis of skeletal muscle cDNA from pigs heterozygous for the SNP and/or SWC9, shows that the same imprinting holds in this tissue in the pig as well (Figure 4). Therefore if *Igf2* were responsible for the observed effect, and knowing that only the paternal *Igf2* allele is expressed, one can predict that (i) the paternal allele transmitted by F1 boars (P or LW) would have an effect on phenotype of F2 offspring, (ii) the maternal allele transmitted by F1 sows (P or LW) would have no effect on phenotype of F2 offspring, and (iii) the likelihood of the data would be superior under a model of a bimodal (1:1) F2 population sorted by inherited paternal allele when compared to a conventional "Mendelian" model of a trimodal (1:2:1) F2 population. The QTL mapping programs were adapted in order to allow testing of the corresponding hypotheses. H_0 was defined as the null-hypothesis of no QTL, H_1 as testing for the presence of a Mendelian QTL, H_2 as testing for the presence of a paternally expressed QTL, and H_3 as testing for the presence of a maternally expressed QTL. Figure 3 summarizes the obtained results. Figure 3a, 3b and 3c respectively show the lodscore curves corresponding to $\log_{10} (H_2/H_0)$, $\log_{10} (H_3/H_0)$ and $\log_{10} (H_2/H_1)$. It can be seen that very significant lodscores are obtained when testing for the presence of a paternally expressed QTL, while there is no evidence at all for the segregation of a QTL when studying the chromosomes transmitted by the sows. Also, the hypothesis of a paternally expressed QTL is significantly more likely ($\log_{10} (H_2/H_1) > 3$) than the hypothesis of a "Mendelian" QTL

for all examined traits. The fact that the same tendency is observed for all traits indicates that it is likely the same imprinted gene that is responsible for the effects observed on the different traits. Table 2 reports the ML phenotypic means for the F2 offspring sorted by inherited paternal QTL allele. Note that when performing the analysis under a model of a mendelian QTL, the Piétrain and Large White QTL alleles appeared to behave in an additive fashion, the heterozygous genotype exhibiting a phenotypic mean corresponding exactly to the midpoint between the two homzygous genotypes. This is exactly what one would predict when dealing with an imprinted QTL as halve of the heterozygous offspring are expected to have inherited the P allele from their sire, the other halve the LW allele.

These data therefore confirmed our hypothesis of the involvement of an imprinted gene expressed exclusively from the paternal allele. The fact that the identified chromosomal segment coincides precisely with an imprinted domain documented in man and mice strongly implicates the orthologous region in pigs. At least seven imprinted genes mapping to this domain have been documented (*Igf2*, *Ins2*, *H19*, *Mash2*, *p57^{KIP2}*, *K_vLQTL1* and *TDAG51*) (ref. 15 and Andrew Feinberg, personal communication). Amongst these, only *Igf2* and *Ins2* are paternally expressed. While we cannot exclude that the observed QTL effect is due to an as of yet unidentified imprinted gene in this region, its reported effects on myogenesis *in vitro* and *in vivo*¹³ strongly implicate *Igf2*. Particularly the muscular hypertrophy observed in transgenic mice overexpressing *Igf2* from a muscle specific promotor are in support of this hypothesis (Nadia Rosenthal, personal communication. Note that allelic variants of the *INS* VNTR have recently been shown to be associated

with size at birth in man¹⁶, and that the same VNTR has been shown to affect the level of *Igf2* expression¹⁷.

The observation of the same QTL effect in a Large White x Wild Boar intercross indicates the existence of a series of
5 at least three distinct functional alleles. Moreover, preliminary evidence based on marker assisted segregation analysis points towards residual segregation at this locus within the Piétrain population (data not shown). The occurrence of an allelic series might be invaluable in
10 identifying the causal polymorphisms which - based on the quantitative nature of the observed effect - are unlikely to be gross gene alterations but rather subtle regulatory mutations.

The effects of the identified QTL on muscle mass and fat
15 deposition are truly major, being of the same magnitude of those reported for the *CRC* locus^{6,7} though apparently without the associated deleterious effects on meat quality. We estimate that both loci jointly explain close to 50% of the Piétrain versus Large White breed difference for muscularity
20 and leanness. Understanding the parent-of-origin effect characterizing this locus will allow for its optimal use in breeding programs. Indeed, today half of the offspring from commercially popular Piétrain x Large White crossbred boars inherit the unfavourable Large White allele causing
25 considerable loss.

The QTL described in this work is the second example of a gene affecting muscle development in livestock species that exhibits a non-mendelian inheritance pattern. Indeed, we have previously shown that the callipyge locus (related to the
30 qualitative trait wherein muscles are doubled) is characterized by polar overdominance in which only the heterozygous individuals that inherit the CLPG mutation from their sire express the double-muscling phenotype⁵. This

demonstrates that parent-of-origin effects affecting genes underlying production traits in livestock might be relatively common.

5 Example 3:

Generating a reference sequence of IGF2 and flanking loci in the pig.

- 10 The invention provides an imprinted QTL with major effect on muscle mass mapping to the IGF2 locus in the pig, and use of the QTL as tool in marker assisted selection. To fine tune this tool for marker assisted selection, as well as to further identify a causal mutation, we have further generated
- 15 a reference sequence encompassing the entire porcine IGF2 sequence as well as that from flanking genes.

To achieve this, we screened a porcine BAC library with IGF2 probes and identified two BACs. BAC-PIGF2-1 proved to

20 contain the INS and IGF2 genes, while BAC-PIGF2-2 proved to contain the IGF2 and H19 genes. The NotI map as well as the relative position of the two BACs is shown in Figure 5. BAC-PIGF2-1 was shotgun sequenced using standard procedures and automatic sequencers. The resulting sequences were assembled

25 using standard software yielding a total of 115 contigs. The corresponding sequences are reported in figure 6. Similarity searches were performed between the porcine contigs and the orthologous sequences in human. Significant homologies were detected for 18 contigs and are reported in Figure 7.

- 30 For BAC-PIGF2-2, the 24 Kb NotI fragment not present in BAC-PIGF2-1 was subcloned and sequenced using the EZ::TN transposon approach and ABI automatic sequencers. Resulting

sequences were assembled using the Phred-Phrap-Consed program suit, yielding seven distinct contigs (figure 8). The contig sequences were aligned with the corresponding orthologous human sequences using the compare and dotplot programs of the GCG suite. Figure 9 summarizes the corresponding results.

Example 4: Identification of DNA sequence polymorphisms in the IGF2 and flanking loci.

- 10 Based on the reference sequence obtained as described in Example 1, we resequenced part of the IGF2 and flanking loci from genomic DNA isolated from Piétrain, Large White and Wild Boar individuals, allowing identification of DNA sequence polymorphisms such as reported in figure 10.

15

Legends to the figures

Fig. 1: Test statistic curves obtained in QTL analyses of
5 chromosome 2 in a Wild Boar/Large White intercross. The graph
plots the F ratio testing the hypothesis of a single QTL at a
given position along the chromosome for the traits indicated.
The marker map with the distances between markers in Kosambi
centiMorgan is given on the X-axis. The horizontal lines
10 represent genome-wide significant ($P < 0.05$) and suggestive
levels for the trait lean meat in ham; similar significance
thresholds were obtained for the other traits.

Figure 2: Piétrain pig with characteristic muscular
15 hypertrophy.

Figure 3: Lodscore curves obtained in a Piétrain x Large
White intercross for six phenotypes measuring muscle mass and
fat deposition on pig chromosome 2. The most likely positions
20 of the *Igf2* and *MyoD* genes determined by linkage analysis
with respect to the microsatellite marker map are shown. H_0
was defined as the null-hypothesis of no QTL, H_1 as testing
for the presence of a Mendelian QTL, H_2 as testing for the
presence of a paternally expressed QTL, and H_3 as testing for
25 the presence of a maternally expressed QTL. 3a: $\log_{10}(H_1/H_0)$,
3b: $\log_{10}(H_2/H_0)$, 3c: $\log_{10}(H_3/H_0)$

Figure 4: A. Structure of the human *Igf2* gene according to
ref. 17, with aligned porcine adult liver cDNA sequence as
30 reported in ref. 16. The position of the nt241(G-A)
transition and Swc9 microsatellite are shown. B. The
corresponding markers were used to demonstrate the
monoallelic (paternal) expression of *Igf2* in skeletal muscle

and liver of 10-week old fetuses. PCR amplification of the *nt421(G-A)* polymorphism and *Swc9* microsatellite from genomic DNA clearly shows the heterozygosity of the fetus, while only the paternal allele is detected in liver cDNA (*nt421(G-A)* and *Swc9*) and muscle cDNA (*Swc9*). The absence of RT-PCR product for *nt421(G-A)* from in fetal muscle points towards the absence of mRNA including exon 2 in this tissue. Parental origin of the foetal alleles was determined from the genotypes of sire and dam (data not shown).

10

Figure 5: A NotI restriction map showing the relative position of BAC-PIGF2-1 (comprising INS and IGF2 genes), and BAC-PIGF2-2 (comprising IGF2 and H19 genes).

15 Figure 6: Nucleic acid sequences of contig 1 to contig 115 derived from BAC-PIGF2-1 which was shotgun sequenced using standard procedures and automatic sequencers.

Figure 7: Similarity between porcine contigs of figure 6 and orthologous sequences in human.

20

Figure 8 Nucleic acid sequences of contig 1 to contig 7 derived from BAC-PIGF2-2, (the 24 Kb NotI fragment not present in BAC-PIGF2-1) which was subcloned and sequenced using the EZ::TN transposon approach and ABI automatic sequencers.

25

Figure 9: Similarity between porcine contigs of figure 8 and orthologous sequences in human.

30

Figure 10: DNA sequence polymorphisms in the IGF2 and flanking loci from genomic DNA isolated from Piétrain, Large White and Wild Boar individuals.

REFERENCES

Literature cited with example 1

1. Andersson, L. et al. Genetic mapping of quantitative
5 trait loci for growth and fatness in pigs. *Science* 263, 1771-
1774 (1994).
2. Knott, S.A. et al. Multiple marker mapping of
quantitative trait loci in a cross between outbred wild boar
and Large White pigs. *Genetics* 149, 1069-1080 (1998).
- 10 3. Edfors-Lilja, I. et al. Mapping quantitative trait loci
for immune capacity in the pig. *Journal of Immunology* 161,
829-835 (1998).
4. Andersson-Eklund, L. et al. Mapping quantitative trait
loci for carcass and meat quality traits in a wild boar x
15 Large White intercross. *Journal of Animal Science* 76, 694-700
(1998).
5. Fronicke, L., Chowdhary, B.P., Scherthan, H. &
Gustavsson, I. A comparative map of the porcine and human
genomes demonstrates ZOO-FISH and gene mapping-based
20 chromosomal homologies. *Mamm Genome* 7, 285-90 (1996).
6. Alexander, L.J. et al. Physical assignments of 68
porcine cosmids and lambda clones containing microsatellites.
Mammalian Genome 7, 368-372 (1996).
7. Rohrer, G.A. et al. A comprehensive map of the porcine
25 genome. *Genome Research* 6, 371-391 (1996).
8. Marklund, L. et al. A comprehensive linkage map of the
pig based on a wild pig-Large White intercross. *Anim Genet*
27, 255-69 (1996).
9. Marklund, L., Nyström, P.E., Stern, S., Andersson-
30 Eklund, L. & Andersson, L. Quantitative trait loci for

- fatness and growth on pig chromosome 4. *Heredity* In press(1998).
10. Ohlsson, R., Hedborg, F., Holmgren, L., Walsh, C. & Ekstrom, T.J. Overlapping patterns of IGF2 and H19 expression
5 during human development: biallelic IGF2 expression correlates with a lack of H19 expression. *Development* 120, 361-368 (1994).
11. Ekström, T.J., Cui, H., Li, X. & Ohlsson, R. Promoter-specific IGF2 imprinting status and its plasticity during
10 human liver development. *Development* 121, 309-316 (1995).
12. Hemberger, M. et al. H19 and Igf2 are expressed and differentially imprinted in neuroectoderm-derived cells in the mouse brain. *Dev. Genes Evol.* 208, 393-402 (1998).
13. Dunger, D.B. et al. Association of the INS VNTR with
15 size at birth. *Nature Genetics* 19, 98-100 (1998).
14. DeChiara, T.M., Robertson, E.J. & Efstratiadis, A. Parental imprinting of the mouse insulin-like growth factor II gene. *Cell* 64, 849-859 (1991).
15. Sun, F.L., Dean, W.L., Kelsey, G., Allen, N.D. & Reik, W. Transactivation of Igf2 in a mouse model of Beckwith-Wiedemann syndrome. *Nature* 389, 809-815 (1997).
16. Davies, J.L. et al. A genome-wide search for human type 1 diabetes susceptibility genes. *Nature* 371, 130-136 (1994).
17. O'Dell, S.D. et al. ApaI polymorphism in insulin-like
25 growth factor II (IGF2) gene and weight in middle-aged males. *International Journal of Obesity* 21, 822-825 (1997).
18. Falconer, D.S. & Mackay, T.F.C. *Introduction to Quantitative Genetics*, (Longman, England, 1996).
19. Hill, W.G. Rates of change in quantitative traits from
30 fixation of new mutations. *Proc Natl Acad Sci U S A* 79, 142-145 (1982).

20. Marklund, S. et al. Molecular basis for the dominant white phenotype in the domestic pig. *Genome Research* 8, 826-833 (1998).
21. Kijas, J.M.H. et al. Melanocortin receptor 1 (MC1R) mutations and coat color in the pig. *Genetics* In press(1998).
22. Beechey, C.V. personal communication (1998).
23. Paquette, J., Giannoukakis, N., Polychronakos, C., Vafiadis, P. & Deal, C. The *INS* 5' variable number of tandem repeats is associated with *IGF2* expression in humans. *Journal of Biological Chemistry* 273, 14158-14164 (1998).
24. Sambrook, J., Fritsch, E.F. & Maniatis, T. *Molecular cloning : A laboratory manual.*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1989).
25. Chowdhary, B.P., de la Sena, C., Harbitz, I., Eriksson, L. & Gustavsson, I. FISH on metaphase and interphase chromosomes demonstrates the physical order of the genes for GPI, CRC, and LIPE in pigs. *Cytogenetics Cell Genetics* 71, 175-178 (1995).
26. Green, P., Falls, K. & Crook, S. *Documentation for CRI-MAP, version 2.4.*, (Washington University School of Medicine, St Louise, MO, 1990).
27. Haley, C.S., Knott, S.A. & Elsen, J.M. Mapping quantitative trait loci in crosses between outbred lines using least squares. *Genetics* 136, 1195-1207 (1994).
28. Churchill, G.A. & Doerge, R.W. Empirical threshold values for quantitative trait mapping. *Genetics* 138, 963-971 (1994).
29. Anonymous. *SAS version 6.10*, (SAS Institute Inc., Cary, NC., 1990).

References used with example 2:

1. Fuji, J.; Otsu, K.; Zorzato, F.; Deleon, S.; Khanna, V.K.;
Weiler, J.E. O'Brien, P.J.; MacLennan, D.H. (1991).
Identification of a mutation in the porcine ryanodine
receptor associated with malignant hyperthermia. *Science* 253:
5 448-451.
2. MacLennan, D.H. & Phillips, M.S. (1993). Malignant
hyperthermia. *Science* 256:789-794.
3. Grobet, L.; Royo Martin, L.J.; Poncelet, D.; Pirottin, D.;
Brouwers, B.; Riquet, J.; Schoeberlein, A.; Dunner, S.;
10 Ménéssier, F.; Massabanda, J.; Fries, R.; Hanset, R.;
Georges, M. (1997) A deletion in the myostatin gene causes
double-muscling in cattle. *Nature Genetics* 17:71-74.
4. Andersson, L.; Haley, C.S.; Ellegren, H.; Knott, S.A.;
Johansson, M.; Andersson, K.; Andersson-Eklund, L.; Edfors-
15 Lilja, I.; Fredholm, M.; Hansson, I.; Håkansson, J.;
Lundström, K. (1994). Genetic mapping of quantitative trait
loci for growth and fatness in pigs. *Science* 263:1771-1774.
5. Cockett, N.; Jackson, S.; Shaw, T.; Farnir, F.; Berghmans,
S.; Snowden, G.; Nielsen, D.; Georges, M. (1996). Polar
20 overdominance at the ovine callipyge locus. *Science* 273:236-
238
6. Hanset, R.; Dasnois, C.; Scalais, S.; Michaux, C.; Grobet,
L. (1995). Genotypes at the locus for halothane sensitivity
and performance in a Piétrain x Large White F2. *Genet. Sel.*
25 *Evol.* 27: 63-76.
7. Hanset, R.; Dasnois, C.; Scalais, S.; Michaux, C.; Grobet,
L. (1995). Introgression into the Piétrain genome of the
normal allele at the locus for halothane sensitivity. *Genet.*
Sel. Evol. 27: 77-88.
- 30 8. Olivier, L.; Lauvergne, J.J. (1967). A study of the
inheritance of the muscular hypertrophy of the Piétrain pig:
preliminary results. *Annales de Médecine Vétérinaire* 111:
104-109.

9. Rettenberger, G.; Klett, C.; Zechner, U.; Kunz, J.; Vogel, W.; Hameister, H. (1995). Visualisation of the conservation of synteny between humans and pigs by heterologous chromosome painting. *Genomics* 26: 372-378.
- 5 10. Goureau, A.; Yerle, M.; Schmitz, A.; Riquet, J.; Milan, D.; Pinton, P.; Frelat, G.; Gellin, J. (1996). Human and porcine correspondence of chromosome segments using bidirectional chromosome painting. *Genomics* 36:252-262.
11. Yun, K.; Wold, B. (1996). Skeletal muscle determination and differentiation: story of a core regulatory network and its context. *Current Opinion in Cell Biology* 8:877-889.
- 10 12. Knoll, A.; Nebola, M.; Dvorak, J.; Cepica, S. (1997). Detection of a DdeI PCR RFLP within intron 1 of the porcine MYOD1(MYF3) locus. *Animal Genetics* 28, 308-322.
- 15 13. Florini, J.R.; Ewton, D.Z.; McWade, F.J. (1995). IGFs, muscle growth, and myogenesis. *Diabetes Review* 3:73-92.
14. Catchpole, I.R.; Engström, W. (1990). Nucleotide sequence of a porcine insulin-like growth factor II cDNA. *Nucleic Acids Research* 18(21):6430.
- 20 15. Feil, R.; Moore, T.F.; Oswald, J.; Walter, J.; Sun, F.; Reik, W. (1997). The imprinted insulin like growth factor 2 gene. Pp70 In *Genomic Imprinting*. Eds. Reik & Surani. IRL Press at Oxford University Press.
16. Dunger, D.B.; Ong, K.K.L.; Huxtable, S.J.; Sherriff, A.; Woods, K.A.; Ahmed, M.L.; Golding, J.; Pembrey, M.E.; Ring, S.; the ALSPAC study team, Bennett, S.T.; Todd, J.A. (1998). Association of the INS VNTR with size at birth. *Nature Genetics* 19: 98-100.
- 25 17. Paquette J, Giannoukakis N, Polychronakos C, Vafiadis P, Deal C. (1998) The INS 5' variable number of tandem repeats is associated with IGF2 expression in humans. *J. Biol Chem* 273(23):14158-14164
- 30

18. Andersson-Eklund, L.; Marklund, L.; Lundström, K.; Haley, C.S.; Andersson, K.; Hansson, I.; Moller, M.; Andersson, L. (1998). Mapping Quantitative Trait Loci for carcass and meat quality traits in a Wild Boar x Large White intercross. *J. Anim. Sci.* 76:694-700.
19. Rohrer, G.A.; Alexander, L.J.; Hu, Z.; Keele, J.W.; Smith, T.P.; Beattie, C.W. (1996). A comprehensive map of the porcine genome. *Genome Research*, in the press.
20. Georges, M.; Nielsen, D.; Mackinnon, M.; Mishra, A.; Okimoto, R.; Pasquino, A.T.; Sargeant, L.S.; Sorensen, A.; Steele, M.R.; Zhao, X.; Womack, J.E.; Hoeschele, I. (1995). Mapping quantitative trait loci controlling milk production by exploiting progeny testing. *Genetics* 139: 907-920.
21. Baron, H.; Fung, S.; Aydin, A.; Bahring, S.; Luft, F.C.; Schuster, H. (1996). Oligonucleotide ligation assay (OLA) for the diagnosis of familial hypercholesterolemia. *Nat. Biotechnol.* 14(10):1279-1282.
22. Lander, E.; Green, P. (1987) Construction of multilocus genetic linkage maps in humans. *Proceedings of National Academy of Science (USA)* 84: 2363-2367.
23. Lalouel, J.M. (1983). Optimization of functions. *Contrib. Epidemiol.Biostat.* 4:235-259.
24. Lander, E.S. & Botstein, D. (1989). Mapping mendelian factots underlying quantitative traits using RFLP linkage maps. *Genetics* 121:185-199.
25. Spelman RL, Coppieters W, Karim L, van Arendonk JAM, Bovenhuis H (1996) Quantitative trait loci analysis for five milk production traits on chromosome six in the dutch Holstein-Friesian population. *Genetics* 144:1799-1808.
26. Chirgwin, J.M.; Przybyla, A.E.; MacDonald, R.J.; Rutter, W.J. (1979) Isolation of biologically active ribonucleic acid from sources enriched in ribonuclease. *Biochemistry* 18:5294-5299

Table 1 Summary of OTL analysis for pig chromosome 2 in a Wild Boar/Large White Intercross¹

Table 1. Summary of QTL analysis for carcass traits									
Trait	F ratio ²	Map position ¹	Percent of F, variance ³	Least squares means ⁴ $\overline{W}P/\overline{W}M$	Least squares means ⁴ $\overline{W}P/LM$	$L P/\overline{W}M$			
	<i>QTL</i>	<i>Imprinting</i>		n=62	n=43	n=30			
<i>L P/LM</i>									
<u>Body composition traits</u>									
10	Lean meat in ham, %	24.4***	19.1***	0	30.6	63.6 ^a	64.2 ^a	66.4 ^b	67.3 ^b
	Lean meat mass in ham, kg	18.1***	16.8***	1	24.3	4.69 ^a	4.72 ^a	4.94 ^b	5.02 ^b
	Lean meat + bone in back, %	12.2**	9.6**	0	17.4	66.3 ^a	66.7 ^a	69.3 ^b	70.8 ^b
	Longissimus muscle area, cm ²	10.3**	4.8*	1	15.4	31.9 ^a	33.0 ^a	34.5 ^b	35.2 ^b
									67.3 ^b
<u>Fatness traits</u>									
15	Average back fat depth, mm	7.1*	8.7**	0	10.4	27.2 ^a	27.7 ^a	25.5 ^b	24.7 ^a
<u>Weight of internal organs</u>									
	Heart, gram	9.7**	11.4***	0	14.4	22.6 ^a	22.5 ^a	23.8 ^b	24.4 ^b
<u>Meat quality traits</u>									
20	Reflectance value, EEL	5.7	6.1*	1	8.1	18.6 ^a	18.4 ^a	21.8 ^b	19.7 ^a

P*<0.05; *P*<0.01; ****P*<0.001

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Table 1, continued

- ¹Only the traits for which the QTL peak was in the *IGF2* region (0-10 cM) and the test statistic reached the nominal significance threshold of $F=3.9$ are included.
- ²"QTL" is the test statistic for the presence of a QTL under a genetic model with additive, dominance, and imprinting effects (3 d.f.) while "Imprinting" is the test statistic for the presence of an imprinting effect (1 d.f.), both obtained at the position of the QTL peak. Genome-wise significance thresholds, estimated by permutation, were used for the QTL test while nominal significance thresholds were used for the Imprinting test.
- ³In cM from the distal end of 2p; *IGF2* is located at 0.3 cM.
- ⁴The reduction in the residual variance of the F_2 population effected by inclusion of an imprinted QTL at the given position.
- ⁵Means and standard errors estimated at the *IGF2* locus by classifying the genotypes according to the population and parent of origin of each allele. *W* and *L* represent alleles derived from the Wild Boar and Large White founders, respectively; superscript *P* and *M* represent a paternal and maternal origin, respectively. Figures with different letters (superscript a or b) are significantly different at least at the 5% level, most of them are different at the 1% or 0.1% level.

Table 2 Maximum likelihood phenotypic means for the different F2 genotypes estimated under (i) a model of a mendelian QTL, and (ii) a model assuming an imprinted QTL.

Traits	Mendelian QTL				Imprinted QTL		
	$\mu_{LM/LM}$	$\mu_{LM/P}$	$\mu_{P/P}$	R	$\mu_{PAT/LM}$	$\mu_{PAT/P}$	R
BFT (cm)	2.98	2.84	2.64	0.27	2.94	2.70	0.27
% ham	21.10	21.56	22.15	0.83	21.23	21.9 5	0.83
% loin	24.96	25.53	26.46	0.91	25.12	26.1 4	0.93
% lean cuts	65.02	65.96	67.60	1.65	65.23	67.0 5	1.67
% backfat	6.56	6.02	5.33	0.85	6.43	5.56	0.85
% fat cuts	28.92	27.68	26.66	1.46	28.54	26.9 9	1.49

Comprises/comprising and grammatical variations thereof when used in this specification are to be taken to specify the presence of stated features, integers, steps or components or groups thereof, but do not preclude the presence or addition of one or more other features, integers, steps, components or groups thereof.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method for selecting a domestic animal for having desired genotypic properties comprising testing said animal for the presence of a parentally imprinted quantitative trait locus (QTL), wherein the method further comprises
5 testing a nucleic acid sample from said animal for the presence of a parentally imprinted QTL, and wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.
2. A method according to claim 1 wherein said QTL comprises at least a part of an insulin-like growth factor-2 (IGF2) gene.
- 10 3. A method according to claim 1 or 2 wherein in the pig said QTL comprises a marker characterised as nt241 (G-A) or as Swc9.
4. A method according to any one of claims 1 to 3 wherein a paternal allele of said QTL is predominantly expressed in said animal.
- 15 5. A method according to any one of claims 1 to 3 wherein a maternal allele of said QTL is predominantly expressed in said animal.
6. Use of an isolated and/or recombinant nucleic acid comprising a parentally imprinted quantitative trait locus (QTL) derived from at least one chromosome or functional fragment derived thereof in the method of any one of claims 1 to 5.
- 20 7. Use according to any claim 6 wherein said QTL is related to the potential muscle mass and/or fat deposition of said animal.
8. Use according to claim 6 wherein said QTL comprises at least a part of a insulin-like growth factor-2 (IGF2) gene.
9. Use according to any one of claims 6 to 8 wherein a paternal allele of said QTL is capable of being predominantly expressed.

56

10. Use according to any one of claims 6 to 9 wherein a maternal allele of said QTL is capable of being predominantly expressed.

11. Use according to any one of claims 6 to 10 to select a breeding animal or animal destined for slaughter for having desired genotypic or potential phenotypic properties, wherein said properties are related to muscle mass and/or fat deposition.

12. Use according to claim 11 to select a pig.

13. Use according to claim 12, wherein the pig is homozygous for an allele at a paternally Imprinted QTL, preferably located at a *Sus scrofa* chromosome 2 mapping at around position 2pl. 7, wherein said QTL is related to the potential muscle mass and/or fat deposition of said pig and/or wherein said QTL comprises at least a part of a Insulin-like growth factor-2 (IGF2) allele.

14. Use of the isolated and/or recombinant nucleic acid as defined in any one of claims 6 to 9 to develop a transgenic animal.

15. Use according to any one of claims 12 to 14, wherein the animal is a male.

16. Sperm or an embryo derived from an animal developed according to claim 14.

17. Use of a sperm or an embryo according to claim 16, in breeding animals destined for slaughter.

18. A method for selecting a domestic animal for having desired genotypic properties substantially as hereinbefore described with reference to the Examples.

57

19. Use of an isolated nucleic acid substantially as hereinbefore described with reference to the examples.

DATED this 30th day of November, 2004

UNIVERSITY OF LIEGE, MELICA HB AND SEGHERSGENTEC N.V.



WATERMARK PATENT & TRADEMARK ATTORNEYS
290 BURWOOD ROAD
HAWTHORN VICTORIA 3122
AUSTRALIA

P19791AU00

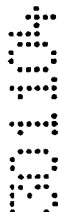
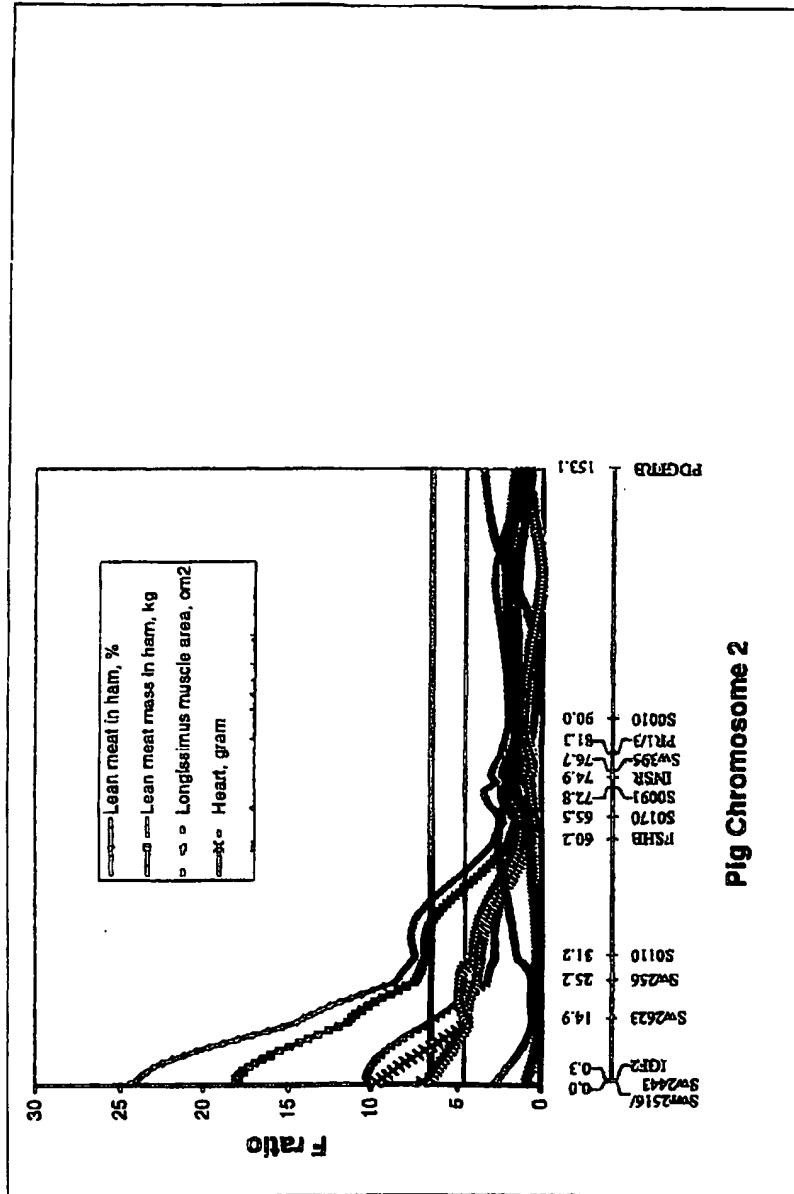


FIGURE 1



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FIGURE 2



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FIGURE 3A

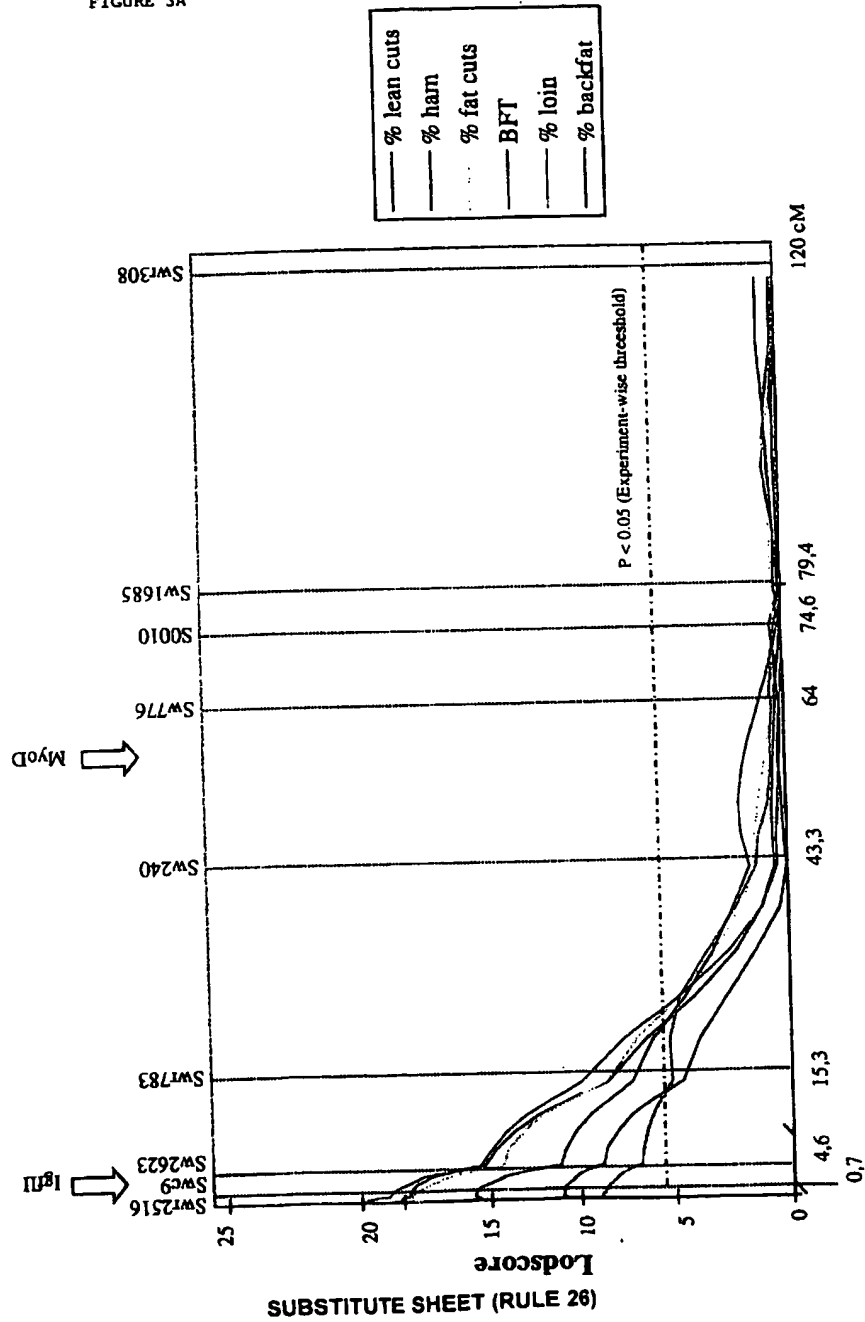


FIGURE 3B

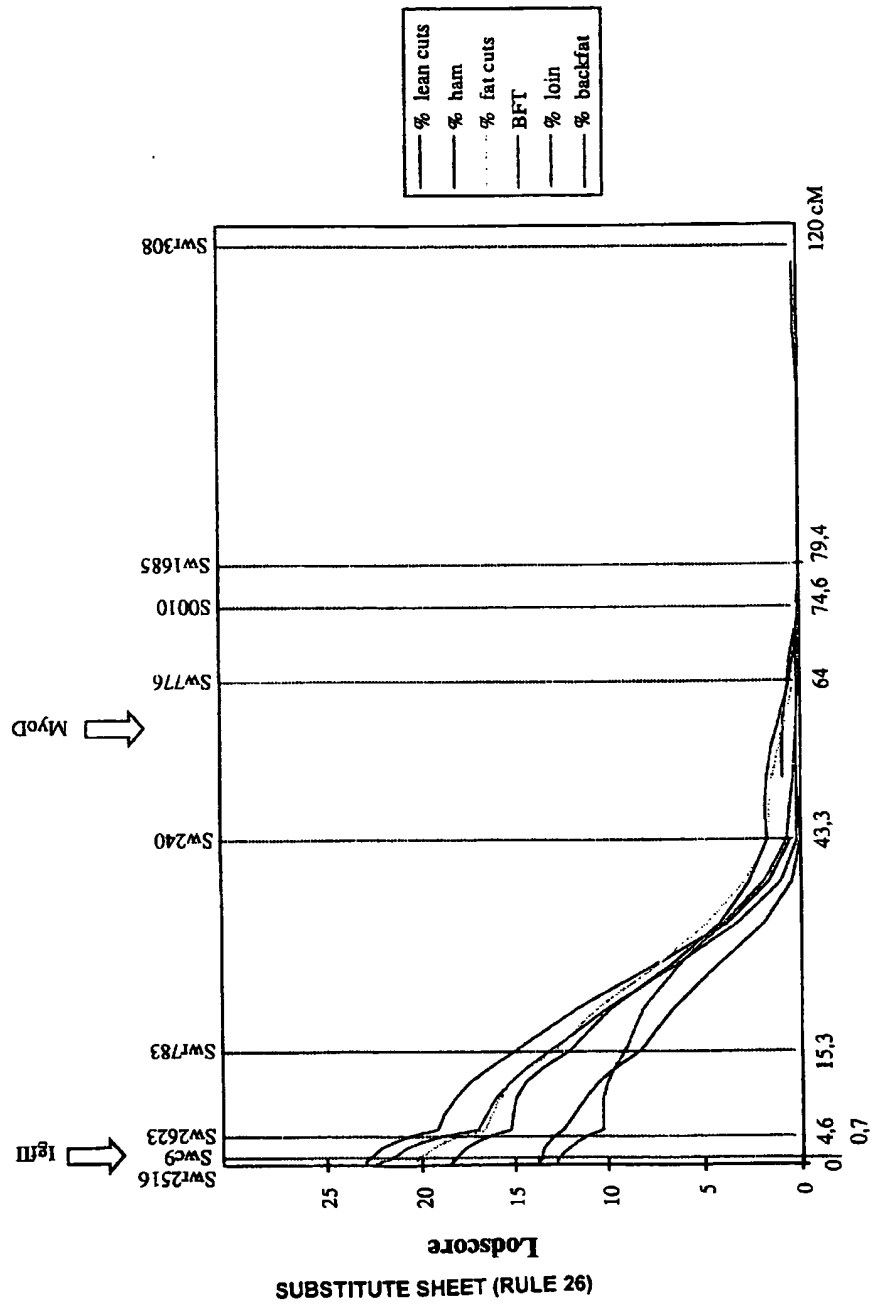


FIGURE 3C

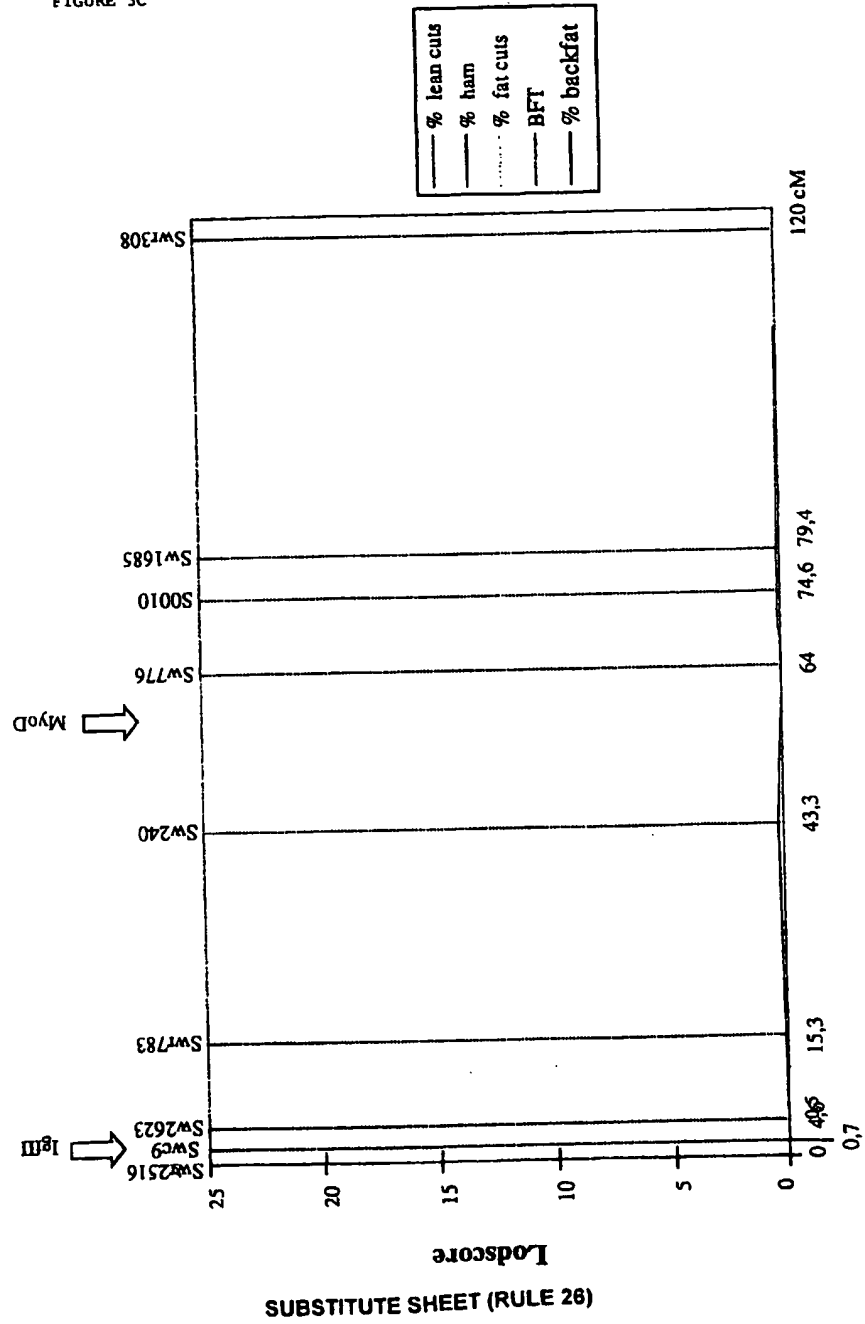
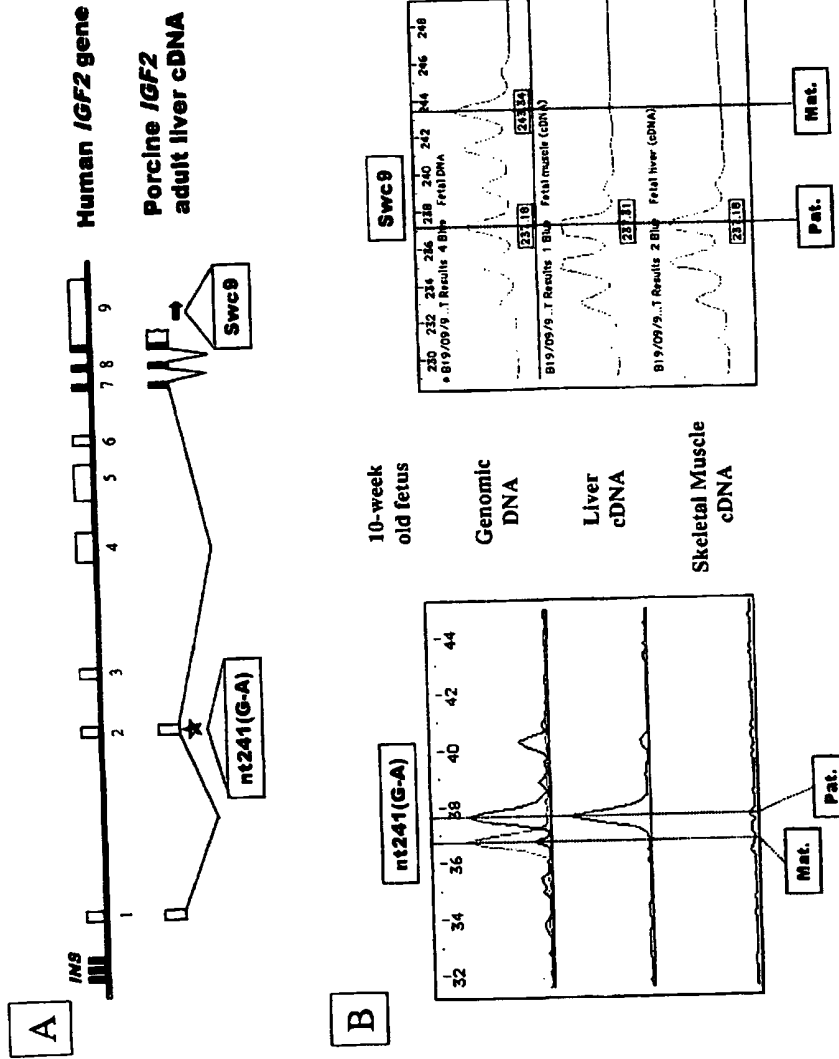
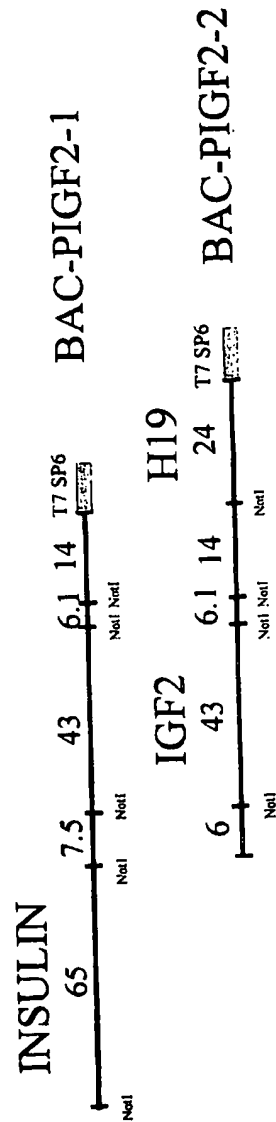


FIGURE 4



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FIGURE 5



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FIGURE 6

Contig 1 (500 bp)

GGGTGGGACGCTTCCTCCAGACCCGAGGAGGCCAAGTTCCCTGGCCCTGCCACCCAGGGCCAGCTGAAGC
AGGTGAGAGACACCCGCTCTCTGCTCCCTGTCACCTAACCCACAGGCCGGGGCCAGGGACACAGGCCACA
TGGCATCTCCCCCATGCCCTGCCCAAGGCGCCAGCAGGTGAGGCTGGAGCAGAGTCTGGGTCTCTGGGG
CCAGACCGAGGGCAGGACAGCTGGGCATCTGTCTCACAGTCCCGCGCTTTGTGGGAGGGCGCAGAGCCTC
ATCCAAGACGCCCAAGGAACCGGAGAGGCGGAGGCGCGGCTGCCGCGTCCAGGCCGGGGAGGCCCTTG
AAGTGGGGGCGCTTGGCGAGCGGGAGCGGAAGGCCCTGCTCAACCTGCTTTCAACCTGAGGGCCACCAAGCC
CCCCCTCGCTGTCCGGTCCCTGAAAAAATTCTAGGTGAGGGGGCGGGCCAGGGCTCCCCGGG

Contig 2 (943 bp)

TGCTCCTCACACCCCGGGCGGGCTGCTTTGGGGCCATCCTCCCATGGGCCACACCCACTCTGGCCTTC
ACACCTGCGCTTCTGGGAAGTCCCTCTGGTCCCAAGGAAGTTTCTGAGCTGGACAAGTGCCACCACTGG
TCACCAAGTTCGATCTGAGCTGGACCTGGACCAACCCGGTGAGCCGGTGCTCCCTCCCCGGCGCCATGTC
TCCCATCCCCAGGGGTGTCCCACTCAGGGCCGGGACTGGGCGTGAACCCCGGGTTGGGACGGATGTTGGC
CTGCTGTGTGGCTCCTGGCGGAACAGAGAGGCTGGCTGGTGCCACCCCAAGGGCCCCCGCGATGACACGG
GCCGCGTCTGGGTGGGCGGGCAGGGCGGCCAGGC
AGGGCAGCCTCCGATGGCGTCCCGGCTGTACCAGGGCTTCTCGGACCAAGTTGACCGCCAGCGCAGGAAGC
TGATTGGCCAGATCGCCTTCAGTACAGCCAGTAAGTCCCTCCAGGGCCTCAGCTGGGGGCCAGACCTCAG
CCTGGGCGCTCAGGCCAGACCTGGGGGTGGAGGAAGGGAGGTTGCTTTGTACCAACGCCACCACTTCACT
GTACCATGGTACCGACTCTGGGTCCCAATACAGCTGAGGAAGTGGGGCAGAGTGGTTAAGCATCT
TGCTGAAGCCACAGCTGGCGGAGCATTTGGCCCCGCCCTCTGCGGCTCCACACCTGCTCCTGAGGG
GCCCGGGACTGACAGCTGTCCCTCTCTCAGAGGTG
ACCCATTTCCTCCCGTGGAGTACACAGCCAGGAGATTGCCACCTGGTGAGGCCCTGTACAGCGGCTGGGAG
GGCGGGAGTGGGGGAAGGGACAGGAAGCTCAGAATTCCCGCTGGAACGTGGTGGCTCTATCATGA

Contig 3 (1500 bp)

GGGGAGGGGATGCTCAGACCCGCTCTGGGAAGAAGAGGCTCAGAAGAAATCCCTTCCCAAGGGTCACGCGG
TGGAGCCAGGGGCCCGCTAGGGGCCGATTCCACAGCTCGTGCTGCCACCTGTGGCGCTCCAGGAACCTGC
GGAGGCGGTGGGGCCCTGGATGGGTCCGCGAGTGGGCTCGCAGGAGACCCCTGGAGGGGCTGGGACACCC
AGCTGCCACTCACAAGTGGCCAAAGCGCGGTGGCAATGGGCTGAGCCTCTCCCCCTCTCTCTCCGAGGA
CATTGGCCCTCGCATCCCTGGGGGTCTCGGACGAGGAATTGAGAAGCTGTCCACGGTGGGTTTCTCCCCCTGC
AGGGCCCTGGGTCCAGCCAGGCCCTCTCTGTCACAA
GGGGTGTCTGCTCAGCTGTGACCGCCCGGAGCCTGGATCGGTTCTGCTGGGTGGGCGGTGCCCGGGCCA
CGGGCAGCAGGGGACGCGGTGCGGGCCCGAGCCGTGTCTGAGCCCTTGGCGCTGTCCCCACAGCTGTAC
TGGTTACGGTGGAGTTTGGGCTCTGCAACAGACGGCGAGGTGAAGCCCTACGGGGCTGGGCTGTCTGCT
CCTACGGGGAGCTCCTGGTGAGGCCCTCCCCACGCGCTGGGCGCTGGGTCCCCGGGGAGGTGACCCCTGCGG
TGCTTGTGGATTCCAGCTCTCGGGAGGCTGGAGCGAGGGGCTGCCCTCTGGGGCCACCAAGAAAGCTGGT
TGCGCCCTCTCCACACACCTGTGCTGGGCCCTG
GGGGGACCCCTGCTGGGGATGTGGGTGCACAGCCAGGGGCCACAGGGAGTCAGGACACGGGGCTCCCTTCCC
TCGGGTCCCTGAGACCCCTGGCTTCCCGCAGCACTCCCTGTCCGAGGAGCCCGAGATCCGGCCCTTCGACCC
CGACCGGGGGCGGTGCAGCCCTACAGGACAGACCTACAGCCCGTCTACTTCTGTCTGAGAGTTTCAGT
GACGCCAAGGACAAGCTCAGGTGGGCCGGGGCCCGGGGCCCAACTGGAGGATCCAGCTGACGCCCGCC
TATGAGCCATTTCAGCAGAGGGAGCTGTGCGGACCCACCGTCACAACCCCTTCCACAGCTGGAACC
CCAGAAAGCTCGGAGGGGGGACCTGCAGGGCTG
TGGCCAGGTCAAGGCAAGTTCAGGCCAGGCTTTAGGGGTGAAGTCTGACTTTGTAAAGGGGGTGCAGGGT
CCTTCCAGCTCTCTCCCTCCGAGCAGCTGGGGCGGGCGGGGTGCGATGAAGGCAGAGATGACGCGAGCC
ACCCGTTCACCTCAGGAGGCGCTCCTGTCCAGCAGGGTCTGTGTGTCACAGGGAACTGAGGCCCGAGG
TGTGTGTGGGGGGGTGATTCTCACACACAAGCTTAGGGACAGGGACATAAGGCGCTCTCCAGGGCACAG
TCTGGAGG

Contig 4 (3024 bp)

TTAANTCCANGTTGGCCCGACAAAGTTTCCCCATTTGAAAAGGGGCCAGTTAAGCCCCAACNCAATTAATTGG
AAGTTAGCTCCCTCATTAGGCTCCCCAGNCTTTACNCTTTATGTTCCGGTTCGTATTTTGTGGGAATTGTA
GCGGATACAATTTCTCTCAAGNAACAGCTATGCCATGATTACGCGGTACAGTAGTTTATCAGTCCCCCGG
CCCATGGGACAGCGAAGGGAACAGTATGTCGTGGGGCCGGGTCTAAAGGGTCAACACAGGGAGGGGAGG
GGCTCCAGGAGGCGAGGCCACTGAGCGGTACCTGGTGGGGGAGGTGGTGGGGCCACCCAGGAGTCTGTG
CCCCCCCCCTCCCGCGTGTGACATGAGAAGCAGGGCCAGCTGCGGGTCCCTGAGTTCAGCGCCCCCCCC
CCCCACCCCGCAGCAGCCCGGGGTCTCAGCAGGCTGCTGTGCTGGGGCGGGGGCGCTTATGGRGCCGGGAG
CAGCCCCCCCCCAGGCTTCAGAGCATCTCTGGGGCTCAGGGATGGACCGGGGTCTGCRGGCAGGTGCTCTC
TCGGCCCCCACTCCCTGGGCTATAAGCTGGAAGATGGGCCCCAAGCCCGGCGGTTTGGCCCTTGTCCCCAG
CCAGTGGGGACAGCTGGCCCTCAGGCCCTCGTTAAGACTTAATGACCTCAAGGCCCCAGAGGGCGCTGAT
GACCCACGGAGATGATCCCGAGGCTGCGACAGGGAATGATCCAGAAGTGCCACCTCAGCCCCAGCCCA

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FIGURE 5, CONTD.

TCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGCGCGGGGGGAGGCGCTATAAGCCGGCCGGGCCAGC
CGCCCCAGCCCTCTGGGAOCAGCTGTGTTCACAGGCCACGGCAAGCAGTCTGTCCCCCTGGGCTCCCGTC
AGCTGGGTCTGGGCTGTCTGTCTGGGGCCAGGGCATCTCGGCAGGAGGACGTGGGCTCCTCTCTCGGAGCCCT
TGGGGGGTGGGCTGTGTGGGGGTGCAGGTGCCCTGGCTGGCCTCAACGCCGCCCTCCCCAGGTCTCAC
CCCCGCCATGGCCCTGTGCACGCCCTCTGCCCTGTCTGCCCTGTCTGGCSCTCTGGGGGCCCGCCCGGC
CCAGGCCCTCTGTGAACAGCACCTGTGCCCTGCCACCTGGTGGAGGGCGTGTACCTGGTGTGGGGGAGCGC
GGCTTCTCTACACGCCCAAGGCCCTGGGAGGGGAGAACCTCAGGGTGGAGCCGAGGGGGYGTCCCGGA
GCGGTGGGGGAGTTTTAAGGAGGAAATTGGTAAAGTGACCAACTCCCTGGGAGCTGAGCCAGAGACACC
CCTCCACGCCCYGGTCCCGCTCGAGAAGCCCCCTTCCCTCCCTCCTCCCG
AGGGGGCTCAGGGAGGAATCTTACGGAGTCAAGGCCGGGTGCCGTGGTCTCCGAGTGACATGGCGTGGT
GTCCCTCTGCCGCCACATGCCCTGAGAGAGGCCCATCCCCCTGGGAGGGGGCCCGTCCCGGCCAGGC
GGCGGGAGGCCAGGACCGGTGGCTGTCTGGCTTCCACTCAGGGTGGGGGGGTGGGGGTGGCTGTCTCT
GTGTGACCGGCTCTCCCCGAGCAGGTGCCCTGGAGCTGGGGGAGGCCCTGGGGGGCTGCAGGCCCTGGCG
TGGAGGGGCCCGCAGAACCTGGCATCTGTGGAGCAGTGTCTGCACCACTCTGTTCCTCTACCACTGGA
GAACACTGCAACTAGGGCGGCCCTGAGGGGCCCTGTCTCCCCGACCCCAAAAGCCAAATAAGTCTGAA
TGAGCCCGGGCGAGTCTGTGGTCTGTGGCTGGGGCGGGGCCCTGGTGGGGAGGGGCCAGAGGCTGT
GGGGGGCTGTCTGCGACCCCTCTCTGTCTCTCGGCACATCGGCTGTCTAAGCTTCTCCACATGCAATCGGT
GCCACAGCCATGCGCACCGGGGACAGGGCCAGGGCAGGGCCCTTCAATGTGGCGAGCTCTGGTTTC
AGGGCTCCAGACACCCCTCTGGGTGCCACTGTCTGCACAGGCTCACTCTGAGGGTCCAGGGCAGCCACCC
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CCCCCGGGGACCAAGACTTGGCCAGCTGCCAGTCTGCCAGTCTGCCAGGCCAAACCAATCTGCACCTTGTCTGAAGTTT
CAGCCGGGCCAGCACTGGGGGGGCCGGGCTTAGAGCTGGGGGCCGGGCCAGGGACTGCACACCCGCCAG
GTGTGACCGGCTCTAGGGGTGGCAGCAGGTCTCTCGCTGGGACCCAGCCAGCTGGGCGAGTCACTCTCAACAG
AGGCTCTCACTGTGTCTGTCTCTCCCCACGGCCACACAGACACCCCTGGGGAGAGTCAAGGGCCCCAGCA
GGCCCCCGCCCTGGAGAGGAGGCCAGGGCTGGGCGGGGTGGCGGGCCGACACTGCAACCCGAAAGGGGG
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GCACCTGACAGCAGTCAAGTACGTGGGGTCCCCGAGTGGTGTGTCTGGGTGCCCTCTGGGAGGAGCGGG
CTGAGCTTGTGTCTTGCACAGGAGAGCCGTGACCACTCTGTCTTCCCTCCCCCAGGGCCAGGCT
GACTCTTTGGGACTCGGGGCCCTGAGCGGCCCACTGCGAGGACTCACGGGTGTGGGTCTTGGGTGAG
TGGGGGCTTGGGAGAGGCTCACTTGTCTGTGGGTGGGAAAGGCTGAGAGTCATGGTGTGACAGCGCCCTC
GGCTGCGGGTGGGGGTCTCCCTTCTCCCGAGCCAGATCCCCGGGTAC

Contig 5 (1730 bp)

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CTGGCTTACGCCCTGGATGACACCTGGCTGAGCGGTGGGTCCCCGTGTGAGGGCAGCCCCACACAGCT
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ACCAGGCAAGTGGTCCGAGCGGTCACTACAGACAGAACCAGCAGAGGGGCCCAAGGCCCACTTTTGACAA
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CACCGCCCTCCGCTGTCTGGAGGAGAGGAGTCCAGGGCAGAAAGATGCGTGGGATGGGGGGGTGGTCAG
GGGTCTGGGAGCTGTGGAACAACAACAGACAGCGAGGTCTTGGGGGCCCGGCCCGCCCTCCGCA
CTGTGTTTCTGGCCGGGTGAGGACAGCGAGGAGATTCCTTGAAAGTGGAGACTGGCGGGGGGCCCT
CGGGTCTCAGCTACCCCTGAGCTAGCCCGCC
ACTCGGCTCCAACCTCCCGCAGGCCCTGGCACGGTCTCCAGGAGTCCACTGAGGGTCCCCAAAGCTGCCAC
CAGGAGTGGGCTGGGTCTGTACCAACCCACCCACCTCCAAGTCTGAGATATG

Contig 6 (4833 bp)

ATGTGAGCTGCACAGCATGAGCCCTCGGCCCACTGCTGTGGCTTGGGACATTGAGGTGTGTGCCGCCAG
GGGACACACACCTTGGCTCTCAGGGTGGCCGTACAGAGGCGGCTGGGTCTGANGAGGTGGGGGCTCTGGGG
ACCGCTGGTGAATCAGGACGGGGGTGATGCCACCTCTCTCTGAAGGTTTGGTGAAGTGGCCCTTCTCTAT
CGTGATGACAATACTGATTTCTGGAAGAGCCAGGTGTTTTCTGAGGCTGTGGTGCACCTCTCCACGTGGCCA
CAAGGTGCCGGCTCGGTCAGATTTGAGAAAGCCTCGGGAGCGGGTGTCTGCGCCAGATTACAGTGTGCT

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FIGURE 6, CONTD.

CCTCGGGGTCTGGGGTCAGGACGTGGTCCCCAGCAGTCTGCTCCAGAGCCTGTCAGTGATGTGTGGGATTTTA
CCGCTAGAACACAGTTTCTCTGATTCTCAGAAACAGCAGATGCTTTAGGAGGGGCGTGCAGGTTTACCTG
TGCTGCANNGCCCCCTGCCACCTGGTCCGAGCCNCAAGACGGCATCTAAAGATCAGTTCTCATCATCAGTTC
CGCAGTGTGGGGTGGGGCAGATGAGAACCTCAGGGCTGGGCGCAGAGGTGGGAGCCCCCTGGACCCCGA
CACTGCAGGGGGGCCCTCCCCCTGTAGGAAGAACAATGTCCTTTGCCACCCAGCCCTCTCCCCAGGGTGGCC
CGAACTGTTGCTCCTAAGACCTCTGGGCTGTGTGCTGTAATTCATATAGTGGCCACCAGGTGTCAGCAGGAGG
CCACTTAAGCATCCATGTGGCGGAAACCTGGAGCTGGGGGTTCTAAGGGTCCCTCGAGTGTCCTCTGAATAA
ATAGGCGCTGACCTGATCCCCAGGAAGGGATAACCTCTCCAGGCCCTAAGAGGCAGTGGGGCAATGAGGTTT
ATGTGTCCACTGTACCCCAAATTTGCTCTTCTTCCCTTACCTGTGTCCCCACCCTGGACGATACACGGA
GTGCGAGGCTGGGGTCACAGCCCTCACAGCCCCAAAGCTGCAGGTCTGCTCAGGGGACCCGAGCTTGGC
TGGTCCCCCTTGGGTCTCCCCACCTGACCCGCTCTGCTCCCTCCCTTTGCTTAAATGCTCTGCGTTTC
AAGGTTCTGATGGAATAAAATACCCCTGCAGTGGTGTGTTCTCTTTGGGGCTGTGCCAGAAGTGGGATTA
GACCAGGGCAGAGCTCAGATTCCACATACTGTGTTAGGGATGGCAGGTGCCACATTTCAGGAGTTTCATTGG
TGGTTTGAATGCTACTTCCGTTTCAGCCCCCTCAGCTGCCACCTCTCAATTTAGGACCCCCCTTTGG
CGGGTTGCCCATGGAACCATCATCTGGCGTGGGGTGAGCCCTTTATCTCCCTGGCCCCACTGGGAGGGTT
TGGGGAAGTCCCAGCTAAATTTCTCGTAGGGACCTGGAAGGAGCCCTTGTGACATCTGGGCACAGATAAGAG
GTAGGGGACACAGGCGGTGAACACTTGAAGCTGCAGAGCCAGAGCAGAGCCAGCAGGAGCAGTGCATCTC
CCCCACCAAGAACTGTGGGTGCGTCAACACTCCCCACTGTGTGCCCTGGACCTGACAGGGCCTTTAGCCT
CCCTGCTCCCTCCCCACCAAGAACCCAGTGAGGCACCCACTTGGCCCTCTTAGTGTGTTATGCTCTG
GGGATCTGCATTTGTTTAGGACACCCAGCTAGATTAAAGTCCCCCAAGTGTGACTCTTTCTCCACTG
AAAACCTGTCTCCCCACCAAGGGCCCTATCCCTTTAGCTGAGCCAAAGGAAATTCAGGAGGGGCTTGAATG
ACAAAGGAAGAGGGGAGAGTTAAACCCCAACACTGGCTGGCAAGCTGGGTGGGAGACCCAGGGTGA
GGGGTGAGTGAAGGTAGCGGCTGGTGGCCCTTCTGGAAGTACATGTGACTTTGCCATTAGGTGAGTCTTTGC
TTTGCCCTGCTCTATCTCAGGCTTATGGAAGAAGTTAAATTCAGGAGCACTTGGTCTAACCCAGGCAGC
GCTTGATCTGGGCCCTTCCCCAGCTGTGACCACTCTGAGTCTGCGCTTAGTTGGAGTTTGGCCAAAGCTC
AAGAGGCTGTGGACCCAGTCTATCCACCCAGGGGTGCTGTGGGACAGGCTGTGCTGCCATTTGCTGTC
AGTATGTCCTGTCGGGACCAACACATGCTGAGGGGTTGATACAGGTGCCACTGGGGAAGGAGAGAAA
CTCCCCAGGTGAGTCCCCCTGCTCTGGAAGCAAGATGGACATGACCGCACTGTGTGCACTGCATTTGGAGGC
CCCGAAGAAAGATTTCGTGATCTTTCTCGAACCTGCTTTTCCCATCATGCCCCCCCATTTTACCCGT
GCCACGCCACTGGTGTGCCGGGTGTCAAGTGAAGTGAACAAGTGTCAATCTACTGAGGCCCTGCCACTCTCC
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TCTGTGAGCCTAGAGCTGGACCAAAATCTCCACCTGTAACTGTGCTGCCCTGGCGTGGGAAGGTGGCAGG
CAGTTGCCCCAGCAGCCCAAGCACTAAAGTTGGCACAAGCTACCCAAATTTGAGGGGGCTTGGGGAAGGG
CATGGAGGGGATGAGGAGGTGAGGGGCAAACTAATTTCAAGTATGATTTGAGCAGGTGCCACGCTCAGCGTG
GAGAGGCTCTCTTGTCTTAGGGACCCATTATGATGCACAGCTAAAAGGCCCTTACCATCTCTCCAGCCT
CAGCTTTGTCCCCCTCTCTCTCAGCGGCAACCCGGCTGGAGGGTCTGGCCACTACAGCCAGAGGCCCCCC
TACTTTGGTGGCACTGCTACTATTGGCCCAACACCGGATCACCGCCAGGCAGTTTCGGCAGAGAGTCTGG
GGCACCAGTGACTCCCCCTCTCTTTATCCACCCAGGAGCTTACAGGACTACACAGGCTAGAGGGCA
GGTAACTGGTCTGCCCTCCCTAGGGCTGCCCTCAGAGTGTGTGAGAAAGCTGCATTGAGTGTGTTGGGTGC
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AAGCTTCGACTTTGGAGGGGACAGGAAAGACAGGTGGAGAGGGGACACTTCCCTCTTCTGTACAGAGCCAC
CCGGAGCCACAGAGGCTTTTGAAGGAAATAGGTTTCCCTCACTAATGCAGCAGGCAAAATGGGAGGGGCA
GGGGTGAGGGGTAGTGCCCCCCCCCAGCAGGAGGGCACAGCTGTTTCTGCAAAATGTAAGAAAGCAGGGTTT
TTCTGTGTGAGAAGTTCCCTCTTGTGCTATGTCACCCACCCCGCCCAAGACAAACAGGACACTGTGCAGA
GGGGCAGAGCCCCGAGATTTGGAGTTGTTTTATATGCATATATACCATTTTGAAGCAAGCTTCCCTCT
CCCCACTCTCTACATGTCCCCCTTACCAAAAAATCCACACGTAAGTGAAGGGGAGTGAGAAGGACGA
CGAAGGGGCACTGTCCCCCTCCCGTCCACAGCGGGACTTAAACGTACAGCTTTTCGCTCCGGACAGTGTGC
CGCCCCCTGGCCCCCTCAGCTCCCTGCGCGGGGGCTGAGTGTGGGGCCAGGGCTGTCTCCAGGCACTGC
ATTATTTTGTGATGAAGTTTGTGTCGGGCCACCCAGGCTGGTGTGGGGGGAAGGGTTCAATGCTCCAAA
GAAGCCCATCTCCCCCTCAGCCACCTTCCAGCGCTTCCGAAGGCAGAGCTGTGTCTCTGCTGTGTGCTG
GCCCTCTCTTCTTATTTCAAGGTGAAGTGTGGGGGAGGAGAAGGTTTATATTGTGTCTGTGATC
CCCCAGGACAGGGCATTTGTGTGCGGCCCCAGCCCCAGGCCAGGATGGGCCAGCTGCCGACAGA
AGGGTCTCCTGCTGCTTGGCTGCAGGGAACCCAGCTCTGGGTGAACCGTGGGCACCTTCTCTCTCATGCC
CTGTATTAAAGAAAGGAGAGCTGGGGGGCCAGAGGCACAGGGAGGGGAGCCACGGCCCCAGGTCTGACAAGAT
GACCTGCGGGCTCTCCACCCAAAGAGTCGGGGTGGGGGGCGGATTTGGTTTGAAGAGAAATAAGGAAC
ACACTCTTTATTTTCCCAAGGGGCCAAGAGTCAACCTGAACTTGAAGACGACAGCCGGATTCCAGCCCC
AGCCCCAGGGCCCCACATCTCTCGGGCTCAGCCGCGGCCCCAGCTGCCCCCCAGCCTGAGCTGCAGAGGC
CAGGGCTGCCCGAGACCCAGCCCCAGGTGAGCTGCTGCACCTCTGGGCCAGGAGATCTCCGCGGGCTCAG
AACTGAGGGCGGGCAGCCACCCAGCCACAGCGGTGAGTGTCTCCAGACCCAGGGCAGGGCCGGTGTCCCC
CGGCACAGAGAGCTGTGCTGAGGCCAGACCTCCAGGCCGTTTAGTTCCCATCTCCCTTGGGGGAGGGG
TGGGCTCAGAGGGGCTGGGGTGATCCGAGAGCTGGGGTGACGGGCTCCAGGTGCCCTCTCCAGGCGGG
TGGCCGGAGGGGG

Contig 7 (2014 bp)

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FIGURE 6, CONTD.

CTGGTTTCGCACTCCTCCGGGGACTGTTGAAGTACCGAGAGCGCNCGCGGAGCGCCGGGGGAGCGGGGGTG
GCCGCCGGGGGTGCTCCCGGGCCCCGGACCGAGCCAGGGACGAGCCTGCCCGCGCGGCAGCCGGGGCCGCGG
CTTCGCCTAGGCTACAGCGCGGGAGCGCTGGGGCGCGGCCGCTGCCGGGAGTCCGCCCTGCTCCTCGGAGG
CGGCCGACCGGGGAGCCTGGGGGACCCGAGCGCCGGGGAGCAGCGCCCGGACAGCGCCCGGGGCGCTCTCG
GCTTCCTCCCTTCCAGCGCGCGCCCGCGCGGGCTTCGGCACCGGGGCGCTCTCAGTGGCAGGAGAAGCG
TGCGCTCCCGCGGGGTGGGGGACCCGAGGAAACC
CGCACCGCTGGAGCGCGCGCGCGCGGCGCAGCGCTCGCGTCCCCGGGGAGGGCGCCACTGCTCCGCGCGCG
CGTCCCCGAGCGCCCGCGCGCTTCCCGGGCGCGCGGGATCCTAACCTCTCTCTCGGTCCGAGCCCGCAT
CCCCAGGGCTCCAGGCCCCCGGCACTTCCCGCTCTCTCCCAATTGCAGACAGCACTTTTCTGGGACCTCCC
AAGGACAGCCTGGCTCCAGGGTCCCCAGATACATTACCAATTTCTCAGATCACAAGTGGGTTTTTCGGGC
ACTAATTCAGAGACCTCAAAGCACATGAGCCCTACTGGCTTCCAGGTTTCCACTAGTGGCTCGGTCC
CCACTCACTGGGGATTGTCTCCAGGCTCTCGC
GGTGTGATCCACCCATTTCGCGCCAGGTCCCGCAGTGCCAAATCCCTCTCTAGAAAACCTTAAACACTGACTC
CTGGCTTCGGGGTGAGGCTGCCAATGTGCTGACTCCCGAGAAGGTATACCACTGTTTTCTGGCATTTGGG
CAGCTTCCCCCAAAACAGTGAAGCTCTTTTCCCGCTCCCATAAATTTGGACGCCAGGGGACCCCAAGCT
TAGCGCCCCGTGTTGGCTCCCCACCGCGAAGCCCTGCTCCTGGGGTTTACGACAGTTTGGGACTTTATC
TGCCAGTTTCCCAAACTGATTGGCCCCAAGCTGGGTCCCTAAATTTAGACAAAGAACCCAGCCCCCCCC
CCCACTCCAGTACAGGAAGCGATGCCCCAGGGA
CCCTCGGAGTTGGAACTGGCTTCCTAAGCTTCCACAAAATGAGGCTTTCGCGCATGGCGCGCTGATGCC
CTTCTGAATCAGAACTCTGCGCTCTGATTCTCTGCTTCCACAACTGAGAGCATGATTCTGTGTCGCC
CAAACTCACTGAGCAAAATCTTTTGTGGGGGCTGCAAGAATAGGAGGCACTTCTCTCCGAGCTCTCCAAA
CTCCCTTGCTATAATCAAGTTCCCTAAAATTAGACAGAGCTTCCAGGCCCCAGAGGCACACAGAGCCATT
ATTGAGCTGCGTTTAAATGATGACAGGACCATGGGTGATGACAGCTCCCCAACTACAAATGCCAGGTAT
CCTTGCTCCAGCCAAAGCCAAAGCAAACTCTTGC
ACAGATCCCATATCTTGTGTTATGTCAAGCGCTTTCGCTGCCAGTAAACAAATAGTCTGAGTGTCTTCTCCAC
CTCATAACTTCGGAATATTAATAAATTCCTGGGCCCCGGAGCTGACAGACAAAGATCCGGGCTTCTTAAA
ATTGAGAACTGATTCCAAATCCAGGCCAACGCCAGACCTCTCCCAATCTGGAGCCCTCCGACTGGACAC
ACTGAGCTCTTAAGTATTACGCGCTGTCTCCAGGCCACCCAAATGCATTCAAAGTGAGCTTTGGTACAGAA
AAGGCACTGATTCTTGGGCTCCAAAGCAGCCCATGCACCCCGAGTACCCCAAACTTAGTCAGCACTTTCC
GGGTCTCCCTCCGCACTGCAAACTCCCAACTGCGG
ACACCGGTCTTTCAGGACCCACCGCTAGACGGTCTTAATCCCTTTTCCCCAGACCTAGATT
Contig 8 (371 bp)
AGATTCAAAACTATTTTTCTGGGCGCTCCAAATGAGGTGCTGCCAGTCTCCAAATAAAGTGGGG
GTTTTTGTGTTGTTGTTTTTGTGTTGTTTTTTTACCTTCCACGAAACAACTCAAACTTTTTGGA
CCATTGATTATGGGTCCCTGACTTATGACCTTGCCCCAAGTCCCCCTAAATGTAGGCCATTTCACGG
CGCTCCCAAAATGAAATGCCCCAGATCCCGCGGAAAAAATATCCCGGGTCTGGAATCCAGGTATTACA
GGCTCGGGTGACACCCCTCTTGTACTAACAGGTTCCTGAAGTTTAGAGATCACTACCTAATGAACA
ATCCAC
Contig 9 (2415 bp)
CCAAACTGGGGCCCTATCTTACTAGGTTCCCTAAATGCAGACAGCGCCCGGAAAAATAGGGCGTTTTTTT
TCCTGTTTCCCAAAATAAATAATGAAACCAATTTTAGAATTAATAATGACCTTGATTTCTGCTG
GTTCTCCAAATGACTTTTACAGCCAGGTTGCCCGAGTTTAGACGGTGTGCTTGAATCTCTAAAGCAC
CTGAGGATTTTCCCGAGGAGCCACCACTACCGAATTTACTGTCTTCCGGGCCACAAGCTCCAGGCC
ACCACTTGATTTCTAAACGTGGAAATCAGCTCCACTTCCCTCCGCGACCCCGAGGGTCTGCTCAGACCC
CCCAACGTGCCCGCTGTTCTTCTCCCCCAATTT
TTATTTAGAGAAATGCTCTCTCGGGTCTGCCAAGTTTCCCGCTGAGACTTCTCGGTCTATCCCAATCC
TCTTCCCCACAGTCCGGGAGCCCCACAAGCTTACCGACCCACATGCTGGGGTCCCCCACTTAAACGCGATC
CCCTGTCCCCAGATTACCGAGTGATTTCCTGCTCTCAGACTGGGACTCTTTACTGGAGTCTCGAATTT
AGCCATTAACTACAGTTCTCCACTCCGACGAGGCTCCCTTGGGTCCCACTCGGGGACATGGGTCTCTTG
CCTGCAAACTCAGGCTGCTCTGACTTGCAATTCAGGCTTTGGGCATTGTTCCCGCGCCCGCGGGTCTCGGT
TCCCCCATCCCGCGCACGAGGGCACTGGGTCTG
GGCTCTTGGTGTCTCTACAAAGTCCCGGAGCTCCTCGGACTTGGGAATGTCTCTTGGTTCCCCAATAC
ACTCGGCGCGGAGTGCTCCGCCAGGACGTAGGCAGAGCTTCTCCCGCTCCAGGAAAAACGACTGGGCATTG
CCCCAGTTTCCCCCAAAATTTGGGCATTGTCTTGGGTCTTCAACGGACTGGGCTTGCCTCCGACATGC
GGACTGCCCGGGGCTCTGCTCAGCTTACGCGGCTCCACCGCCGCTGCAGAGCGCTCGCTCTCGCTCTC
GGTCCCGAGCGCTTGGGGACGAGCTCCGGGCTCCAGCTTGGGTGAGCTCCCGCTCGCTCTCGGT
CCCGGCCGGCTCCCAAACTCACTCGCGCGCTCC
CGCTGGGGTGGCACTGGCTCCGCGACTGCGGGGACAGGGAGCGGAGCGGGAGCGCTGCTCAGGCCA
GCCGCTCGGCGGGGCGCGGCCCTGAACGCGCGGCTTCTGTTGCTCTTTGCAAGGTCAACCGTGG
GGAAACGCTCGGCGGCCCGGAGCGGGGAGGCGGCTTGGGAAGGAGGACCGGGAGAGGAGCAC
CCGCTGGGGCGGCGAGCGCGGCGCTCCAGCGCGGGGAGGATCCGGGAGGCGCGCGGAGCGCGG
CGGAAGTGATTGATGGCGGAGCGAGGGGGGAGCGGATCGGGGCTTCGCGCGGCGCGGCGGCTTCCCTCG
GAGGACTCGGGCGGCCGGGTTCCTGGGGCGGG

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CGGGGCGCGGGGGCTTGTGCGTGGTCTCCAATTGGTAAAAATACAACGACTTTTACGTGCGCCCGGACTCTC
CAGGAGATGGTTTCCCGAGGCCCAAAATATTCTGGTGGGCCCGGGGCTGAACCCGGCTTACGCAAGGCC
AACGGCTCAGGACGGGGGAAACCAATTCCGATATTTTGGTGGGCCCGCAAGCGAGCTGTTAGACGGCG
CGGGTGAGCTCGGTCTGCAGGTAGGCTTGAGCGAGGTTCCCGGCCCTGCTCTCTCTTCGGGAGCGCG
CCGGGAGCGCGCGCCCTCCACGACTGCGACCTTGGCGGCCCGCGAGACGACTCCCGGTTCCCGCGCG
CACCGGGGGCGCTCGGGCTCTGGCTGGGCTCGA
GGGCTGGCGCTGCTCGGGAGGTTGGAGGCTTACCGCGGGGCCCGCGCGAGGACACCCCTTACCCCGAG
GTCCAGGCGGACTCGGGGCGCCCGGATCCAGGCTTGACCACTGTGCCGACCGCGGGAGGCTTGTGA
GACTTACCACCTGGCGCGCCCGGTCCCCCGGCACGAATGTAGGATCTTGACACCSCCGGAACCTAAGAC
GGGCGCCCACTACATCTTCTGACAGGATTTCGGATTCTTCAAGATCTGCAGATCTGTATGCCAAATTTGA
TGGCTGCATTATTCTTGTGATAATTACGCAAAAGATGGCGACCAGAGCTATGGCGCTCTGGGTTTAAAGG
GAACCCAAATTAACGATCTGGTCAACGAACAGAT
AGACATACGTTTT
Contig 10 (3753 bp)
AGATTCAATGGGGATCCGATAGGAAAGCCCTGCTGCTGCTGCTGCTTCTTTGGCGTTGGGCTCTGGTCTG
CTATGCTGCTTACCGCCCACTGAGACTCTGTGGCGCGGGAGCTGCTGACACACCTCCAGTTTGTCTGGGG
GATCGCGGGCTTACTTCTAGTAAGTACGTACGCGGGGACGGGGGGGGGGCGGACACAGAGGTTGCTTCATCT
GTCCGCGCCCGGACTCTGTGGGCTCTTCGGGATGGATGTTGGGACGCGGGGGCGGGGGCGCGCAAGG
CAGGACTCTCTCGAGGGGTTGAGATCTACAGCGGGGGCGCCCTGGCCCTTCGCGATGATTGTGACCATGCG
CATGTGCTTGCTGGGCTCACACCCCTGAGCTTCTTCAGCGTACTCGAAACGGGAAACGAGGAGCGAG
GTGGCAGCGGGTGGGAGGCGAGCCGTGAGTGGCAGGCGTGGAGGGGTTCTTTCGGCGGGGTGCGCCAGCG
AGGCCCCACAGGATCAGACGCTTCCCCCTCTGCTCTTACCTTGACCTGCCACGACAGGGGCTGACGAGCATG
ACATTACCCTGATTTGTGGTGCTGAGCTCTTGGCAGTGGCATGGTTGTTCTGAGCTTGTGATTTGAAAG
TGGAAATAGATGGGTTAAAAACCAATAGAAATAAAGGCCGCTGTGGCTGGCGCATCTCGCAGAGAGTGACCG
TGCCCTCTCTGGGTTGGGCTTTGGGTGGGTTCCATAGGTTGGGCGGGCGGCATGACGAGGTTGGCCCTGCG
TGCCCTGAGAGTCTTTGGCGCTTCACTTCTTCTCTGCGGCCCGCTCCGCTCTGAGGCTGGCTGGCTGGG
CCCGGAGAGCTCCGCTCCCGCTCTGCTCTGTGCCAGGAGCAGGTTGAGCCCTCTCTTGGGCTTGTGCTG
CACCTCCCAGCAGGCTGGGCTCAGTGTCTTACCTGTAGGATGGTTCAGGGGCGCTCGGAGAGAGTCTCG
GGACATGGGAGGAGCTGGGGGAGGGCGAGCTGACCTGAAAGTGGGATGTTGTCTCTCCCTTGGGCTGACG
CAGCCGCGCTTGGGCGGGAGGGGGTGGGGACGTGGCTGGGGGCAAGTTGTCAAGGGCGCGAGGCTCACCC
CGCCCATCGCTCCCCATGTGGCAGCTCTTCTGACGCTCTACTTACCACCTCTGAAATGGGCTGAAAC
ACCCATCTTGGCATGCGAAAGGTTCTCTGTAAAGAGGCTGGTCTGTTCTATGCTCTTGAGGCCCTGCTG
CCCTGGGCTCTGAGCCCTCTCTCTCTGCTGCTTGTGGGGCAGGAGTGGCACCATAGAATCTGGCGCTGGG
CCTGGGAGCGGCCCTCTGTGGCAGGCTTCCCCGAAAGGAGGGCTGGGCTGAGCTCCCCACCTCTGGACCC
TCTACGAGACCTCTTACAGGGGCTTCCCCCCCCCCCCCGCTGGCGGGGCTGGGCTGGGGGCTTTT
CCTTGAGGCCGAGTCGGAAGCTGTGCGAGCGAGGCGGAGGACGAGGAGAGAGGAGGGCGGCTGTTTCTGCTGGT
CTCACTCTCTCTCTCCGCTTCTCTCTCTCTCTCTCCATCTCCACCTGTGTCTCGGGGCTCGGGGCGGAG
GTCGCGCAGGGGCGTGTGATCATTGGGAGCCGCACTCGGCTCCCGCTGGGCTTTCGGTCTAGGCGCACGGC
CCACTCTTTTCAAACAGGCTTGGGTCTGAGCGCCCAAGAGGCTGGGCGGCTTTAAGGACGGGAGGAGGGC
CCAAGAGGCGAGGGCTGGTCCCGAGCAGCCCGCACCGCTACCCCGCTTGTCCCTCTCTCTCCCGGG
GGCCCTCTGTGACCCCACTCTACTTCTTGTCTGCTGAGGCGCAGGAGCTGGCTTCCCCGACAGGTTACCGGG
GCTCTGTCTGGAGGCGGGGCGGGGCGCTGGGCGACCTCGTGGCGGGGCGCTGTGCTGAGCTGTG
CTCTCCCTCTGTCTGTGGAATCTTCAGGAGCGCGGACCGCGCTGCAACCGCCGACCGGCTGAGCATCTGGG
AAGATGCTGCTTCCGATCTGCGCACTGGCCCTGGCAAGCTCTGGACACTTACGCAACCCCGCGCAAGTCCGAG
GGAGCTGTGACCCCTCCGACCGTGCTTCGGTAAAGGACGCCCTCTCTCGGAGCGGCCCGCCCGGGGGG
GGCTGTCTCTTGAGCGGGGAGCGGGGCGAGCGGCGCTTGGGCTTCAAGTCTGCGCAGAGGGCTCTT
CCCGCTGGGGCCCTGCGCAAGACCGAGGAGCTCTGCTCTGCGAGGAGTGCAGCAGGAGGAGCCCG
CAGAGCTGTGTTCTTGGGACAGGGGCTGGGGGCGCAGGCGCCCCCTCTGACCGGCGCTTCCCTCTCAGGACA
ACTTCCCCAGATACCCGCTGGGCAAGTTCTCCGCTATGACACTGGAAGCAGTCCGCCAACCGCTCCGACG
GGGCTTCCCGGCTCTGCGCGCGCGCGGGGCTCGACGCTCGCCAGGAGCTGGAGGGGCTCAGAGAGCC
AAGCGTACGACCCCTGCTCGCGCGCTCGCCCGGACCGGACGACCCGCGCCACGGGGGCGCTCTCCGAGGGCT
CGGGCATCGGAAGTGAGCCAATTGTGTAATCTCGGCTGGACCATCACTCTGTGAGCTCTCTCTTCTGACG
GGGAGGCTTCCATCAGGCTCCCTCTTGAGATCTCTGTATACCTTCTCTGCGGGCATCTCCGCCCGGGGCG
CGTGGCGCAACCTCCCATCTGACGCTAGTCTCTCTCGGCCCTTTCGCTCGGCGAGGAGCATCCAAACCA
CAAACCAATTGGCTTGGTCTGTATCTCCCCCAAATATGCCCCCAATATCCCAAGTTACATACCAAAA
TTGAACCTCTCAACCCAGCCACATACACTGACGCCCTGAAGACGAATTTGGCATCTTTAAAAACAGAAAGA
GGCAATTAGCTTTAAAAAAAATAAATACCAAAAATCAATTAGTGTGAAAAAATAA : TACTAAAAAATAATTG
GTTAAAAACATTTGCAAAATAAAGAAATTTGGGCCCCCTCTCTCTCTCTTCTTCTGCGAGCTTGAGTTA
AATTGGCTGTACCAATCTCAAGAGAAAGGAAGGACCAAAATTTGAGTAGGAGTCTGTGCGGCTCAGAC
CCATCTCCCTCTCTGCGACACCTCTCGCGGCCACTGGCGGTTGGACCAAGAGCCAGTCCCGTCTCTC
TCTAGTCTGCTGACAGACCGCGGTGGATTGGCTGGGAGCCCGTGAGTACAGGAGGGAGGACCGGAA
CCGAAACCCCAACCTGCACAGGTACACATGACTGGCCCCGCGACAGCCAGAGCTCTCATCTAGTCTC
CACTTAAAAAGCACTGTACCCACAGCATCTCTCGAGAACAACACACACACACACACACACAGCGACCA
CGACACACCGCGCGACGCGACGCGACACACACTCATGCTATACACACACACACACGACGACGCGGCA

-71-

FIGURE 6, CONTD.

CCACACACACATGCATTACACACACACACTCGTGCATACACAGTGGCGCGCACACACACACACA
CACACTCTCTCTCTCTGTGGGATCCCTGAG
Contig 19 (500 bp)
TGGCTCTGGCATAGGCTGGCAGCTGCAGCTCTGACTGGACCCCTTGCCTG
GGAACTCCATATGCCGTGGAAGCGGCCCTAGAAAAGGCGAAAAA
AAAAAAAAAAACAAACAAACAAACAAACAAAGCCAAACACACAGAACTC
ACAGACACAAGAGAGACTGGTGGTTGCCAAAGGTGGGTCGAGGGTGGG
AAAAATGAGGAGAGGGGGCAAACACACAAACGTGCAGCCATAAAATGGT
AAAGTCCCGGGGACCTCCGGTAGCGCTGTGGGACTCGGGTTGAGAAC
CACCGTGATGTATTCCGAGTTGCTAAGAGTCCCTGTTGGAGAAACAA
ATGGGTATCGACGTGTGGAATGAAAGTTAACCAGCTGCTGCTGTGAT
CACTTTGCAACACATACAGACATAGAATCATTATGTTTACCCCTGGAGC
TGACAGCGTTATACGTCCCCAGCCTCAATTTAAAAACAGCGTTGCCGTG
Contig 20 (400 bp)
TTCATACTGTGCAATGCCAGCCTTAAATGCACAGAGGAGAGCATTAACTT
TTTGCAGAATCACTGAAATGATACCACTCATGTTTTCGAACCTTGCACTT
GGGCGTTATTTTATTTGGTGGCGGAACAGCGCGGATGTGGCACCACCTAG
CGCCGCTGTTTTTATTTCCCTCGGTATCGCGCTCTCGCTGCTTCCCTC
CCCTTCCGCTTGACGCTGAGGAAAGGGCTGAGAGGAGGAAGTCTGCATT
CACCCATCTCCCCCTGCCTCTGTTGTCATCCTTCACAGAAGTGGTGGCCT
GTGGGGGAAGTCACTAAACCTAGGAGGTGTCCCGTGGGGTCTGCTTG
TTACACCTTTGTGCACTGGCCCCAAGTTCTGGGTGGAGCGAGAACGTGGC
Contig 21 (559 bp)
AGCTAGCCCCCAGCCAGGGGCCAGGCTCTCTGCCCACCCGCCAGCCA
GCATGTCTCAAGAGGAGGGGGCTCTAAGGGATGAGGACCTGCTCCAGTC
GGAGACACGAAGCCCCCGGCTCTCCCGAAAGTCCAGCTGCGGCTTT
CGAGCACGGCTGCGCCCTTCGTCAATCATTTAGCCACAGAAGTGAAGG
CGCTTTCGTGGCCGAGGCGAGGCGGACACAGAATGGAATCCACCCAGA
GCGAAGAGCCGCGCTGGGTGAAGCGGCTCTGTGGTGGGACCGGGCGGG
AACTTCACATGGGGTGGCTGTCCCATCTCCCATCTGCTATTACTGCAG
GGGCTCGGCCACACCCGAGCTGCGGGGGCAGTGTGGACACTGGACCT
GGCTCCGCTCTATGATGTATGAGGGGGGGGCGGACAGGGGAGTGGC
CACACCTCGGGCTCCAGCACAGCCAGGATGCGAGAGGGCCCCACCC
ACCAGGGGCATGTACATCCAGAGGACAGCTGAGCAAGCTTGATANG
GGCTTCAAC
Contig 22 (450 bp)
CGTGAGGGGACCCGTGCGGGCTTCCTGTGGCCACAGAGAACAACACAC
CATTATCTTCAGCCCCACCGCGCGGCTTTAATGGGTAACTGGGGCAA
GGGGGCCCTGCTGAGGCGGGGTGGGAGCGCAAGCATGGCTGTGT
GCCCCAGCCAGTCTTCAGGGCGCTGCTGCTGACCCGGGGGCCCCAG
GAAGCAGAGCACCCAGCTTCTCCCTATTCTAGAACCAGCCCCAGAAC
CTGGACCAGACCCAGGCCAGGGGATCTGACAGAGCCACGGCAAGCGG
GCCACTCCACACCCACAGAGGGGGCAGCAACCCAGTCACTGCGCAGC
CCATGCCAGGGGCGAGTGGGACACGAGAGCAGCCCTCATCCACAGCAG
GCAGGGGAGTGAAGTGGTCAAAACGGGGCGGTTCCACGAAGTTAAGCA
Contig 23 (535 bp)
TGCCAGAGACCTCAGAGCTGGGCTCTGCCTTCCCGGGCTGACACGGAGGG
CTGTGGCTTCCACCACCCAGGCCACAGCCAGCCTGCCAAGTCCCTGAA
GTGTCCCAGAGGTGGCCCTGCCTCCACGCCAACATCAGGCTGTGCA
GCCCTGGACGGCCCCCTGTCCCCGGAAGCCCTCGGGGCTCTCTCGGCTC
GGCTCTGGGGAACCTCGGTAAATGTGGCCAGCCGTGCAAGTGGCCGGATC
ATTTGCTCAGGGGGGCCAAGGCCAGGGGGTGACACATCCGCAAGTACCG
CATATGCACAGGATATGGATTGGGTGTGGATTAACTTTTCGCAATGT
CTCTGCCGTACAAATATTGTTTCTAATCTCTGCTCCCTGAGCGCGTG
AGTCTGCCCGGAGCTGCGGGGAGCTGGCTTGTGAACCTGCCCTGGCCC
CCACCCCCAAGGAGCCCCCGGCCAGTGTGAGGGCAGGAAGCTTGGGCA
CAGGCTGCAGAGGCCAGCGCTGGCTCAGTACCT
Contig 24 (868 bp)
TATTGAAGACCTATCATGAGTTCCAGAGCGGAGGGGTGAAGCAGGGG
CCTACAGCCCACTCCCATCACTCCAGACCCGTCCGGGCTGGTGTCCC
TGCCCCCTACTCTGTCTGTGGTGGCGGACGCTCGAAGGAGGCACTGTG
GCCTGGAGCCTGGAGGGTCCCTGAACCTCCCGCTGCCACTGGGCCCTCGG
GCTCTCTGCGCTGGGACCCGCGGTGGTGGGAAGCAGCCCTGCTCAGTG
GGAGGAGCAGGGCTGTGGCGCCCGGCACGGCCCTGGGGGGGACGCACG

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FIGURE 6, CONTD.

CAGGACGCANGTGGGCGTGTGTAGTCCGTCTACACGTCCAGCCAAGGGC
GGCCGCGACCGGCCAGGGTGGGCGAGCCCGAGCCTCAGCAGGGCGCTCTCT
GGGGCTCAGGCTGCCGCCAGGGAGATGAGGGGTGAGGCGCAGTCTGGGG
CTGCTGCCGAGAACCTCGCCAGCTGGCAGCTGGGCACAGGAGACCTG
TACTCCAGAACCTGAGGCTGGACGTCCGAGACCCGCGTCCCGGCTCTT
GGGTGCTTGGTCAGGCTCTCTTTCTGGTTTGTGGGCAGAACCTCTCTAG
CGCGTCTTGCATGGGGTGCTAATCAGGAGTAAGGAGCCAGAGAATGAG
GCACGGAGTATCCAGTGTAAACCTGGAGTATGGAGACGGGAGTACTAAT
TGTGGAGCATGGCTCTAAGGAATGGAGTATTCGTACGGAGAACGCGGGG
CCGGGTGAAATACGGAGAGCGCGGTACGGACAACGGGACGGGGTATCCG
AAGGGGAGGATGGAGTATCGGCCGAGGGGTGGAGAATGGACACTAGAGGA
TGTATANNNGGCGTCAAT

Contig 25 (500 bp)

ACCAGTTTCGATGAGCAATCCAGCGGCGTAACATTATGGCTGCAGCCTG
GTCAATGCGGGTGGAGTTTGAACCTCCACGCGTGGCGATTGTGGTAGATA
AATCGACATGGACAGGGAGTTGATTGAACATACCGGTAAATTTGGCATC
CTTATCCCGGGCGTTGCAGCAACTAAGTGGAGTGGCGGTGGGAAGTGT
GTCCGGGCGTGATGAAGATAAATTTAATTGCTATGGCATTCCGGTTGTGA
GAGGCCCGGTATTGGTTTGCCTCTGGTTCGAGGAAAATGTCTGGCGTGG
ATGGAGTGTGATTGCTACCTGCGACTTCTGCGCAAGAAGAAATACGACAC
GCTGTTTGGCGAAGTAGTATCAGCAGCGGCGAGACGCGCGGTATTGTGCG
AAGGCCGCTGGCAGTTTGTATGATGATAAGCTCAATACGTTGCATCATTTA
GGTGTGGGACGTTTGTACCAGCGGCAAGCGTGTACGGCGGGTTAAGC

Contig 26 (900 bp)

ATGTTTGTATGTCCGCGGTGCTGTAAAAATTTACGCTGCTCGCGTTCTTT
GGCTTCGTCCACCCAGCGAAACGGACAAAATTTCCGTCATACCTTTT
CTTTAGGCGGAAGCCAATGTCGTAATCTTCAGTAAGACTCTGCACGTGCG
AAAGCAATACCGTCACCGTCAGCTAACAGTGGCGTCAAGCGCGGGCGGT
GAAACAGGTGCCGACCGCTGCGTGGGCACTTGTCCGGCAGGGCTTCAC
GCACCGGAACATCTTTGCCATGCGAGCTCTGAAAACATCATCAATGTAAGTC
ATGCTGGTGAAGTGCCTCATTCGCGTTTCGAACGGATACACCGGGATCTG
AATCAGATCTTTACGCTCGACAGATAGTTGAACAGACGCAATTCATCG
GTGAAATCACATCTTCGCGCTCATGCAAGATAAAGCAGCAAAAGCGAAA
TTGGCGCTACGCTCAAATGGGTGATGGCGTCCAGCACGTTGTTACAGACA
GTCGGCTTTGCTGGTGGGGCCAGGACGCGCGCAGACTACCTTATGCACAT
TCGGGAAGCGAGCGCACACTTCGTCAACATCAGCGTGAGTATCGGGGTCG
TTGGGGTAGGTGCCAACAAAGATATGATAGTTTTCGTAGTCGAGCGTGGT
CGCCGCCAGCTCGGCCATATTGCCGATGACGCCCGTTTCATTCCACGCCG
GAACCATAACTCGCTAACGGTTTTCATCTGGTTTATACAGTTTCGGGTAA
CTCATTCGCGGGTAGCGGCGATAAACACTCAACTTGCCTTTAATGCGGCG
TACCCAGTATACGACATCTATAAAAAAATCGTCCAGCCCGCTGATGAACA
TGATGACCGCTAACGTTATCGCGATTACTTTAAGCCGTATAGCCAGGTA

Contig 27 (500 bp)

AGCTGGATGCCCCAGCTGTGGTCCCTTCCTTCCTCAGGGCAGGTTCT
GTCCCTCTTGCGAGCCACCGTCACTGCTGTGGACAGGTCTGCACACCCGCC
GTCCACCAAGAGCGTGGCAGGTCCCTGGGCACGGGCCGGCTCCTGACGCA
CCATGTGTTCAAGGCAAGAGCACTGGACAGAGGGTCCAGACGTCCCTTG
TCCTGCTCAGGCTGGGCGGGGGCAGCCCTGGCGGGAGAGGCCCTGGGCA
TCAGAGCCTCTGTGGCTGGAGCTTGGCGCCCTGCCCTCCACCTCCGT
CTGTCTCCTCGCCGCGCTGCACGGACCTCTCCCGGCCCGCCAGGCTCATT
ACTCTTAAGGACCTAGCCCCCTATGCTGAAATGCTGTACCTCGTGCTTG
TTTTCATCTGTTTATTACCTTATCTTCATTCTGCTGATGATATCTGGT
TATTCTTTATTGATTATATATCTTGTGCTGTTTATAGGACACTGT

Contig 28 (450 bp)

AGTGGGTCGGGCGCTCCTGACGCTCAACACCGTATTTCCAGCGGACCGC
GGATTCAACCTGGTCACACGGACGCCATGTAGACATGTTCCGGGTTACGC
GCAGAGAAGCGACCTGCTCAACCGGCTGGTGAAGTCGGGCGCTCTTCGCCC
AGACCGATGGAGTCGTGGGTGTAAACCATCACCTGACGCTGTTTCATCAG
CGCAGCCATACGTACGGCGTTACGTGCGTATTCACGAAACATCAGGAAGG
TGGAGGTGTACGGCAGGAAGCCACCGTGCAGGGAGATACCGTTAGCAATC
GCGGTATACCGAACTCGCGAACCGGTAGTGGATGTAGTTACCCGCGAGC
ATCTTCGTTGATTGCTTTAGAACCAGACCACAGGGTCAGGTTAGACGGCG
CCGGGTACGAGAACCGCCGAGGAATTCGGGCAACAGCCGGACGAACGCT

Contig 29 (450 bp)

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FIGURE 6, CONTD.

TCAGGCCAATCTGTCTGCTCCAAATGGGACAAATTTGGTCTTTAGGCT
TCTGTCCAATGGTCCGAATGGCCCACTCCCGGGCGCCGCCAAGGGTCC
TCTGTGCTCGGGTGGGCTGGCACGGACGCCCCAGGGTCTGCCAGCC
CCGTACCCGGGGCCAGAAAGCTTCGGGCTCTAGCTGGCTAGTCGGGCTG
CTGTGCAGGGGGGCTGCGCTGGGGGAGAGGCGGGGTGAGGTAAACCTC
CCAGCCGCCCGGGTCCCTGCCGAGCCCTAGGCGCCGAGACGGTGGCTG
GGTCGGTACCGCCAGACCCGAGGGCTCGGGGCCCGGGTACCCAGCTG
TCGCACACGCTCGAGCTCTTGTCTCATCAGGGCTCATCCCTCTGGACC
TCTCTACTGCCCACTCACCCCGCTGGACCCATGAAGCCCCGCGGA
Contig 30 (600 bp)
TAAAACTAGCTCTAGTAGAAACATTTTATTTAAAAATAAAAAACCTGACT
ACGTGCGGAGTTCCCGTTGTGGCTCAGTGGTTGACGAATCCGATGAGGAA
CCATGAGGTTGCGAGTTCCGATCCCTGGCTCGCTCCGTGGGTTGAGGATC
CGGCGTTGCCGTGCGCTGTGGTGTAGGTTGCAGATGAGGCTCGGATCCTG
CGTGGCTGTGGCTCGGGTGTAGGCGGGCGGTACAGCTCTGATGAGACCC
CTAGCCTGGGAACCTCCACATGCCCTGGGAGTGGCCCTAGAAAAAGGGCA
AAAGACAAAAAACAAGAAAAAGAAAAATAAAATAAAAAAGACTATGT
AAATGAAATTAACGACTGCCTAGGGTGGGATTTACAGCATGGGAAGTACA
GCATGGCCGTGACAGTGAAGGCTGAGGCGGGAATAAGAAATAGGTTAG
GTGAGTTTCTCTGCTATTGTGATGTGGTCTGCTATCGCTGAAGACGG
ACTGCACTGAGATAAATGTACAGTAAGCATCCGAAAAACGCCAGAAC
GGCAAAACGAATGACTCCAAGTAAGAACCCAAAGAGAAAAAGGAATAAT
Contig 31 (450 bp)
GCGCGGGCGTTCCGGCTGGGTTATTTAACGTGGTCACCGSTTCGGCGGGC
GGGTCGGTAACGAACAGCAGTAACCCGCTGGTGGCAAACTGTCTGTT
TACCGGTTCCAGCCGAAATTTGGCCGCCAGTTAATGGAACAGTGCAGGAAAG
ACATCAAGAAAGTGTCTGCTGGAGCTGGGCGGTAAACGCCGCTTTATCGTC
TTTGACGATGCCGACCTCGACAAGCCGTGGAAGGCGCGCTGGCCCTCGAA
ATTCCGCAACGCCGGCAACCTGCGCTCTCGCCCAACCGCTGTATGTGC
AGGACGGCGTGTATGACCGTTTGGCGAAAAATTGACGAGGCAATGAGC
AAACTGCACATCGCGCAGGGCTGGTAACCGCGTCACCATCGGCGCGCT
GATCGATGAAAAATCGGTATCAAAAGTGAAGAGCATATTGCCGATGGCG
Contig 32 (450 bp)
GGTGGATGCTGGCGATAGCGTCATCTCGCTTATGCCGTGCAGCGGGCAA
GGATAAAGCGCGCGATAAATGACCCGCGCATCAGCCCATGCCCGCAGA
GTACGGATTACCTTCCCGGTGAGCGCCAGCGTGTATGCGTGCAGCGCGT
GATACGCGCGCTAAAGCGATGGTGGCGCTACGTTTGGTGGCGCGCGG
GGGATTTTACCGCGTTTCCACCGCTTCGGAACCGGTGTAACAGCAG
CGTTTTCTTGGCGAAATCGCCCGCACCTTCTGATTCTAATCTCGCACA
GCTCCAGATACGGCTCGTAAGCAGCACCTGGAAGCAGGTGTGCGACAGT
TTTTTCAACTGCGCTTCCACCGCGGCCACCACTTCGGATGCAAGTGCCC
GGTATTGAGCACCGTAATCCCGCGCGGAAATCAAGATACTACGGCGTT
Contig 33 (500 bp)
ACGTGAGGTTTGGCGGAGGAAAGCGGGGACGAGCAGCCGAGAGGAGTG
GGGCTGGCCTGTGGCTGATGAACTCTGAGAAAGTTAAGAGCCCCATT
TTTGTCTTCTCTTTTATTATGAAAAATTCAAATGGATGCAAAAGTC
CCAAACCTAACTGGACATCTTCTGGTACCAGGAACGGTCAGGCACTTAT
GATGCACCGAGCCCCGAGGGAAAAACCTGCCGTCTGGAGCCACGGTC
CAGCAGGGCACACAGGCCCCAGCCCGCAAGCGGCACGGCTGAGTCAGTGA
ATGGCGTGGCCTCTGGTCAAGGACGGGCACTTGGACCCGAGGGAAGCCT
CTGAGGAGCCCCCTTCACAGCGTCAAAAACTGTTAACAGGGCCATGTTGC
CACCCGCCACACACGTGGTTCAAGAGCAGACCCAGGCATCGTAATATG
TCATCCGTGAGTTCCCTGTGTGCCACCAACAGAAAGCCCATCGTCACGTT
Contig 34 (400 bp)
CGGCATCGATGTACATGGTACGCAAGGCACTCGTAAGGCCCGAGCCTCT
AGGCCCTTGTCATGTGTCAGTGTCTGCTCGCGGGGATCAGCAGCCAGGCTTG
TGACCCCGGCCACTTTGACAGATAAGGACACAGAGAGGCCACAGCACTGG
TGTAGGGCCCCACAGCCAGCAGCCAGGGCAGGGAGGACTGGGTCTACCC
TGCCCTCAGCTGGGCCAGCCTCTCTGGGAGTCCCGAGTCTCCCGAGCTT
AGGAGTGTCCCTGGAACCTCTTCTCTCCCTTCCCGCCTCACCCGGAC
CCCTGCTCCCCCCCCACCAACCCCTCCCTCTCTTTCACCTTGAG
CTCCCTCTGAGGACCTCTACTGTTCTGCTTATCTCCCTTTGAGCCA
Contig 35 (500 bp)
TGGCGTGAACTATGTCTGCGTGAAGACATTTGTGGTGGTAGCGCGT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TATATGCGGGAAGTTTAGCGGAACCTGGACAGCCTGGGTTTATCCGGTAGC
GAAATCCGCTTTACCGGTAAAACGCTGCTAGCGCTGGTGGAAAAAGCGCA
GACATTGCCGGAAGATGCCCTTACCGCAGCCGATGCTTAACCTGATGGACA
TGCCGGGTTATCGTAAAGCGTTTAAAGCGATTAAAGTCGCTGATTACTGAC
GTGAGCGAAACGCATAAGATCAGCGCCGAATTGCTGGCATCGCGTCGGCA
AATCAACCAACTGCTGAACCTGGCACTGGAACCTGAAACCGCAGAACAATT
TGCCGGAGCTGATTTCCGAGCTGGCGTGGTGGAGCTGATGGCGGAAGCATT
ACACAATTTATTGCAGGAATATCCGCAGTAAATCTTCCGAAGCCGAGCT
GGGCGGCTCAGCGCCACATCCGGCTTCGGCAAACTACAAATCCAACACC
Contig 36 (500 bp)
GATTTACAAGCCTGACCCACGCGAAATGCGCTAACAGCGTAAAGTCGT
GCGGCCAGAATTTTTTCGTCTCTTCGCTTTGCGTCAATTCAAAAGTCAGC
GCTACGCCATCAGCATCTTCAATGATGTGATTTCAGCGTCCACGGCAGGTT
GCGGCGAAAACCGTGCGCAGGCAGACCTTGTGTGCGCGCGGACCAAAACC
ACGGCCAGCAAAACCGGTACGCCACCGCAATAGCGACGCCATTTTGAAC
GGTGTGTGTGTGCTCAACACAGAATCTTCTTCAACCCGAGGTTTCCA
CGAGAGAAGGTGTGCGCCCTGTAATGCAAAAGAGGCTTTTACCTGGGGAT
GATCGACCAATGAGGTCCAGTTTCATCCAGTTTACGACGGGAGGAGACA
GGGAGATTGTGTGATGACCGGAAGGGCAAAATTTTCTTAATCATGAC
GCAGTCTTTAACTTCATTTTATCAGGTAAAAAAGAGCGACCGAAGTC
Contig 37 (300 bp)
ACCTGATCAGGCTCTGCACTGTGTTTCATCAGCGGAGCCGAGATTTTGAC
CGCCCCATGCATAACGGAAGGCGTGGGTAACCCCGGGCGGCTTCTT
TATCAAGATGACGTTTCGAATATTCGGCAGGTGCAGTTTGTATTCCAG
AAAGCGGTGAGCGCGTATGAATATAATTCTGTGGGATTGAAGCATCCT
TTTCCCTCCTTCGGTGAATGCGCTGAAACGGCTTATTCAGCGCGTTCA
GGGTACGCGTGATAATTTGCAATTTAAATACCATTATTTGGGTACTTTT
Contig 38 (450 bp)
ATCCTTTTGGGCTCTGGCAATTACGCAATAAAGAAGGCCCCCATGCGATT
AAAGTCACCGGCCACTGTCGTCTAATCATGGAGAAATGTCATCAGTG
CGGTCTCGATGCGCAGGGGATGCTCTGCGTTTCTGGTGGGATGTTAGCG
AAAACATTGCCAGTGGTCAATTAAGTGAAGTGCTACCGGAATATTACCAG
CCAGCGAAGCTGTGTCCTGTTATGTTTCAAGGCTGGCGACGTCAGCGAA
AGTGGCGGATAACGGTAGAGTTTACGCCAGTATTTGCGGAGCACTACC
GGAATGTTTCACTGTGATGCTGATTTATGATTCAATTATCGGGTTGA
TATCAGTTTAAACCTGATTTTCTCCTTTCTAAGCCGCTACAGATTGGT
AGCATATTACCTTTAATCGCGCATGATCTAAAGATAATTGAAGAGGTTA
Contig 39 (450 bp)
AATGTACTGGCAAAAAGCCAATGGCGAAGCGTGGGGAACGTTACATGCTC
TGCTGGCGGATATTAATAGTCAGGGTCAGGTGCAGATGGCGATGAACGGC
GGCATCTATGATGAAAGCTATGCGCGCTCGGTTGTACATCGAAAACGG
TCAGCAGAAGGTGGCGTTAAATCTCGCTTCAGGTGAAGGGAATTTCTTTA
TCCGTCCTGGCGCGCTGTTTATGTGCGGGAGATAAAGTCGGCATCGTT
CGTCTGGATGCCTTCAAAACCAAGTAAAGAGATTCAAGTTGCGGTGCAATC
AGGGCCAATGTTGATGGAACCGGTGTAATTAATCCGCGTATTCATCCCA
ACGTGCGCTCAAGCAAAATTCGTAACGCTGGTTGGGATTAATAACATGG
GAACGCGGTGTTTTGTTGAGCCAGCAGGCAACAAATTTTATGATTTTG
Contig 40 (400 bp)
GACATTAATCATTTCAAAATCAAAGCCCGGTTTCCATCGCCCGTTTGG
TGGCGTGGCACTGAACGCAATCGTTACGAGTGTAATAGTAATGCGCATG
ATTCTGATTTCCGTTTAAATGAAGATACGGCGCATGATACCGCTCGGG
TTGTCTCTCTGTGATACAGAGATACTAGATGTAGTTGAAAAAGATTCA
ACCACACAATATATAGCCAGTAGGGGTGAAATTAACCTGGATATGAGC
GTGACGGGTAGGGGATTTTGTGATTACCGGCAAAAAGAAACCCG
AAGACAGGCTTCGGGGTCAAAGACGCGTATTTATATCATTTTGCATA
CGATTTGCGCATGCTTAACAGTGGCGGATTAATATCTACCGCAGCTG
Contig 41 (500 bp)
GCAAAATCACGTCCGCGACCTGGCGTTGTGCTGGGCCATATTGGCAAAG
GAGCTGGATTGCGGTGCTGCAAGTGCCCTGAATAATGCCATTGTCCTG
TACCGGAAGAAACCTTTCGGAATGAACCCACAGCAGCAGCTAAGCA
GCAGCGTGCTGAGTGCCACGCTTAAGGTACGCCACGGATGATTCAGCACT
TTCCCGAGTCCACGACCATAGCGGCGATTATCCTGTGCAACATTTTTC
CGAGGCACGGGAGAGCGGTTCTGTTTACGCAACGACTCCTGGCTGAGCA
TCCGCGCGCATCATCGGTGTAGGGTCAGCGACACACCGCTGAGATC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AAAATCGCTACCGCCAGGGTAATAGCAAATTCGCGGAACAGTCGCCCCGAC
GATATCGCCATAAACAGCAGTGGGATCAACACCGCAATCAGTGAGAAGG
TCAGCGAGATAATGGTAAAGCGATTTCACCTGCCCGCTTGAGCGCCGCC
Contig 42 (400 bp)
AGCTATCTACGGCAAAAGGCACGGTAGTCAATTCGTTGTTAAATACATC
AAGCGTTTGGCGCCGAAATACCATCTGCCAGATGCCATTTCAATTCGTAG
CGCACTGCATAACGGCTACCGGATGCAGTACGTCAAACCCGAACCTGGGGC
CGGAAGGATTTAGCTTTCTGCAATACACCGCGGCACCACTGGTGTGGC
GAAAGGCGCGATGCTGACTCACCGCAATATGCTGGCGAACTTGGAAACAGG
TTAACGCGACCTATGGTCCGCTGTTGCATCCGGGCAAAGAGCTGGTGGTG
ACGGCGCTGCCGCTGTATCATTTCCTGACCATTAACCTGCCTGCT
GTTTATCGAACTGGGTGGGCAGAACCTGCTTATCACTAACCGCGCGATA
Contig 43 (450 bp)
GATTAGCGCCAGATGCTCGCCATCGAAAAGTTGAATCAACCCAGCTGCG
GGTAATAAGTGCGCGTACGAACAAATTCAGTATCCAGGGCTATCGCCGGA
AAGGCACGGACGGCTTCACACAAGAGCCAGCGCATCGTCCGTGGTAAT
CATTGGTAATTCAAATTGTTTCTCTTAGTGGCGCTCAAAAAAACGC
CGGATTAACCGCGCTCTGACGACTGACTTAACGCTCAGGCTTTATTGTCC
ACTTTGCCGCGCGCTTCGTACGTAATTCGTGCGAAAATTTTCGAC
GTTAGATTTCCGTAACCTCATCAGAACTCCACCAGCTTCGGTACTTTGT
ATCCCGTGAGCTGACGGCGGCAAAAGTCACCACTGACTCTTCGGTAAGC
GATGGATCTTTTTCATCGAAGATTTTACCGCTTACCACTGGAGCC
Contig 44 (750 bp)
GAGCAGCCCCGCTGATGACAGGCATGCGCCCGCTCGGCTCTCTCTCT
GGTGCACTGAGTCACAGGATGGCGCGGTGGGCGCGGTGGTGAAGCGGT
CCTGGAGGGCTCGGGAGGGAGGATGCGCTCAAGCTGGCTCCCGTGGGGC
TGGCCCGAGTAGCCTCCGTGAGGGCACCGTGTCTGCTCCAGAGCCGC
TCCCGGCGCTGCCCTGCCCTCCCTTCCCTGCCCGAGTTCCCGGAGCCCC
TGGATCCCGATGGGAGGCGCCCCGAGGAGAGGGGACAGGGAGGGGGCC
AGAGCTCTGAGGCCACAGACCTGGCCAGGACCTTCGTGGGAAGAAGAG
GTGGGCCCCAAAGGCACCTACAGAGAGGGAGGCTCTGCTGGCTGGGGGC
CTTCCAGGCGGGCTTCCAGCAGGGCCAGTGTCTGGGGGTGGAGGGA
GTCCCTGGCTGCTGGGGGGCGCAGGAGCACCTGGGGCTCTGGGAAGAG
AGCGGAGGAGACTGGAGCCAACTGGGGGACAGAGGAGGGTCCAACCC
CAGCGGTGGTGTGGGGGTGCTGGTGGAGGGCTGAGAGGCTGTGCT
GGGGGGCAGAGCGGTGCTGGGAGGGGAGAAGGGTCCCGAGGCTCATG
GGCCCTTCGAGCAGTGGCAGTTGGGTGGGTGGCTGTCTTAGGGCTGT
ACCACGGTGGGTGCCCTGGAGAAAGAGTCTACCCCTAGTCTTTGCTGCA
Contig 45 (300 bp)
TGGGACCCCCACTCCAGCCCCACTGAGTGACGCGCCCCCTGTGGTCCCA
CCGCCAACCTTGCCTCACACCAGAGGGGTGTGGCCACACCTTGTCCACA
GCCTGTCCCTGAGACCACGAGCCCCGGGTGCTAGCCCCCTCCTCACCCCT
GGACCGAGGAGAAGCCCCACCTGGGCTCAGCTCTTGGAGCTAAACTTCC
AGGAAGGTTCGTGTCCTCGGGTCTTAGAGCATGGTGGGAGGGGGATG
CTGTGGGGGCGCAAGCCCTCCCCACATTTGCACTCGACCCGGTGGNG
Contig 46 (300 bp)
CCGGCTAGAAGCCACGAGAGCCCCAGGCCCGCCGACGTCTCTCTGTC
AGGGATTCCGCAGCCCTGGGGCCACAGGGCTGAGCAGACCTTGGGGTTC
CGGTGTGACTCCAGCCAGGGTCTCTACTGTGTAGGCACAGGGCAGAGTC
AGCCCTGGGACCATGGCCACAGCTGCTCCCGCTGAGCCGGGCCCGCCG
CCAGGCTGGGCCCCCTCAGTGCACTGTCCCAAGCCAGCTGCTCTCCAC
CTCCACTTCTCCATCCAGTCTGCCCCACGGCTTTGCTCAGGCCAG
Contig 47 (500 bp)
TTGACTGGCACTAGCACGAGCTCTGTACCCGGGATCTGGGCTCGGGAGA
AGGGAGACCCCCACCCGGCAGGCCGAGGGCGCTGTACACCATGACTCT
CAGCCTTCCCCACCCGACGGAAGAGTGACCTCTCCCAAGCCCCCACT
CACCAGGACCGCACACCCGTGAGTCTGCGAGTGGGGGCGGCTCAGGG
GCCCGAGTCCCAAAGGAGTCTGCTGGCCCTGGGGGGAGGGGAAGCAGC
AGGGTGGTACGGGTCTCCCTGGTTGGCAGGACCAAGCTCAGCCCGCT
GCCTCCAGAGGGCAGCCGGACCAACCAAGTCCGGGACCCACGTACC
TCAGTGTCTGCAAGTGGCCCTGCTGTACTGGTGCATGGGGCGCTGG
GTGCTCCCATGGACAGCTCGCCACTCATCCAGCCGCTACCCCTTCC
GGGTCCAGTGTCCGGCCGCCACCCGCTGCCAGCCCTGGCCTCCTCTC
Contig 48 (500 bp)

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGGGTTGCCGAGGCTGCTGTGTAGGTGCGAGCCAGCTTGGATCTGGC
GTGGCTGTGGCTGTGGCTGTGGCTGTGGCATAGGTCAGCCACTGCGACTC
CGATTGACCCCGAGCCCGCACTCCACATGGCACAGGTGCAGCAGGG
AAAATAAATAAATAAATAAATAAAGGTGAAGACAGTGGATTTCATCTCT
TGGGGTTGCGGTAAGCTCTACACAATAGGGAGTTTACCATTTCCTGT
TCAAGTGGCACTGAGTCAGCTCAGTCCTGAGGGCCACAGATGCCGTC
TGCCTGGGAGATTGTCTCTCACCACACTGCCCTCTGTCCCCACTAAA
TACTCACTGCCCTCCCGTCCCAAGGGCCCTGCCCCACCTCTGCTTCC
TGTCTCTGAACCTGTGGCCAGCAGCGCTGTGGTGAACCTCACTCTTC
GGCCCCATTGTGCGCACCCCACTGGCTCTCCCCGGCATGGGCAGAN
Contig 49 (600 bp)
GGGATATTGGGGGCATATTGGGGGGAGATCCCCACAAGGCATTGGG
GTTTGTGGTTTGAATGCCCGGGCCGATGGAGGGGCGGGGAAGAA
TCTAAGCCTTACTTGGGGAGGTTGGGCCCGGGCCCGGGCCGAAAT
GCCCCCAAGACAGAAGGTGTACAAAATTCTCAAAGGGTGACCTTAAT
GAAACGGGTCCCGTTGGAAAGAGGTCAACAGGGTGGATTGGTGGCAGCG
CAGAATTACGACATTGTGGCTCTTCCAATGGCCGACGCTGGGGAT
AGGGCCCCCGTGACGGCGGGCTCTCGGTGGGACGGCGGTGAGGGT
CGGTGACGCTTGGCTCTCTGACCGCTCCAGCTCCTTGGCGAGCGTGGC
AGCGCGCGGGCGCGCAGGAGGGCGCGCAGCGCCCTGCGCAGGCGTTGG
GCGGACTGCTTCCAGGTGTCTATAGCGGAAGAACTTGGCCACGGGGTATCT
GGGGAAGTTGTCTGAGAGGGGAAGGGCCCTCAGGGGGGGGCTTGGCCC
CCAGCCCCGTCCAGAACAAACCTTTGCGGGTCTCTGCTGCTGCC
Contig 50 (179 bp)
ATCTTCATATTATGACAGAACTCTCTGCTTCTATCTTGGGGAA
AAGGACGATGTCACTTATGCAATAAGCCCACTTGTGGCCGGGGCTTGA
CATTATCTCTCTGCTGCTGCTGCTGACCGTATTGAACTGAGTTAATGG
GCAATTGATGAAGTAACTGCCACC
Contig 51 (500 bp)
CTCGGGCTGCTTCCAGGGGCTTGGGGAGCCATAGAATGCTATGGAGCA
AGAGAGTGCTATGGTCAGACGACTTGGGGGAAGGTCTGGGAGAAGAGGG
GTGACTGGCCACTGTGATAAAGAGTGGGCGCTTCTTGAGATAACACGGT
GGGCGCCGAGGTGGACCTGTGACAGTGGAGAAGGCTCTGCGCGGGCC
AGTACGTGGCTTGGGCTGCCGGACAGAGAAAGCCCACTCCACGGCTG
CCTCCAGGGCGGCTTCTCTCTTCAACCGCGGGCCATGCCAGGTGC
AGGTGCCATCAGAGGGTGTCTAAGAGAAGCTCTGGGCTGGGGTGTCCCA
GGTCCCGGAAGCCCGTGTCCAGGGGCACTGAGGAAGCGTGGGCGCA
CAGAGACTGTCCCTCGGTGCTCAGAGGGTCCCGTCCCAAGGCAACGA
CGCCCAAGGCGGAGGTGGTGGAGGCTTGGGAGGAGGATGGCCGCGCA
Contig 52 (900 bp)
TGTGTTGACCTGTGCTGCTGCTGCTAGAGGATCAATACTCCTTA
CATAATTAAAGGAGAACAAATGGAACCTTAAAAAATTGATGGGACATATT
CTATTATCCCGATTACAGACAAGCCTGAAAAATGGAACATAAGTTATCG
GATATTCTACTGTTGACTATTGTGCCGTTATTCTGGTGCAGAAAGGCTG
GGAAGATATAGAGGATTTGGGGAACACATCCCGATTTTGAAGCAAT
ATGGTGATTTGAAATGGTATTCTGTTACGACACCATTTGCCAGAGTT
GTATCTGTATCAGTCTTGCAAAATTTACGAGTGTCTTATTAAGTGGAT
GCGTGAATGCCATTCTCAGATGATAAGACGTCATTGCAATTGATGGAA
AAACGCTCCGGCATTTCTATGATAAGAGTCGCCGAGGGGAGCGATTCTAT
GTCAATTAGTGGTTCTCAACAATGCACAGTCTGTCATCGGACAGATCAA
GACGGATGAGAAATCTAATGAGATTACAGCTATCCAGAACTTCTTAACA
TGCTGGATATTAAGGAAAAATCATCAACTGATGCGATGGGTGCCAG
AAAGATATTGACAGAGAATACAAAAACAGGAGGTGATTATTTATTCGC
TGTAAAGGAAACAGGGGCGCTAAATAAGCCTTTGAGGAAAAATTTTC
CGCTGAAAGAATTAAATAATCCAGCGCATGACAGTTACGCAATGAGTGAA
AAGAGTCACGGCAGAGAAGAAATCCGTCTTCATATTGTTTGGCATGTCCC
TGATGAACCTATTGATTTCAGTTTGAATAGAAAGGCTGAAGAAATTAT
GCGTGGCAGTCTCCTTCGGTCCATAATAGCAGAACAAAAGAGGCTC
Contig 53 (450 bp)
CCAGCCACGAGCTGGACCTCCCGAGAGGGGCTGCTCTCTTCCCGC
CCAGACGCCCCCAGCAATCTGTGGCCAGAGGGAGTGATACCGAAGATG
GCCACATGGGGCGCCAGCCACAGGGAACCCAGGAAGGCGTGGACCG
TCAGGAGTCAGGGCTGCTGTGACCCATGTGGCTGGGGACTTCCACAG
CCTGGTGGAGATGGCCGGCACACCGCTGCTCGGGGAACGTGCACACG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GGTGGTACATGTGGCCGGAGCCAGGGCACAGGGTGAGGGGAGAAGGGAG
CATGCGGGTGCAGACTCGGAGCCCGCGCTGAGGTGCTGGGTCTCAGGA
CAGCCTCTGGGAGTGGAGGACCCCATCCACGCCCTCACCAGTGTGTGC
CCGCTGCTCCCCGGAAACCTCAGAGACAGAGGGGCACCCAGCCCC

Contig 54 (1133 bp)

ATGGCGCTCATTAGAATTGACCTCGGTACCTTGGGATCTTTGACCCCT
ACCTCAGCCATCTACAACATTTACCTCCGAATGAATGAGAGACACCAAA
AGCAAAATTCATAGAAGAGAAAAAAGTAACTGGACTTTAAAAATGTAA
ACTTGTGCTCTTAAAGGCAGTGTCTAATGAAGTTCAAAACAAACCACA
GACCATAAGAAAAACTTGCAAATCTTGTCTGACAAAGACTAGTGTTC
GAACATACGACGATCAGGGAGAGGAAAACAGCAATCCTATAAACTGGA
CAAGAAATTTGGGGGAAAAAAACCCACTTGGCCAAGAGTTGGTAAATA
AGGCCATGAAAAACATGCTCAACATCATGAGTCATTAGAAAAATCAAATT
AAATATAATGAGATACTACTACACAGCTATTGAATGGATAAAAAATG
TTTTAAAACTGATTATACCCAGGTTTGGCAAGAACATGAGAAACGAGAT
TTTCACACAGGATTGGTGGAAAACAGAAAATGGTCCACCCACTTTGAAA
AGAGCTGGGCACTTCCCTCAAAAGTTAAACATACATCCAGGACCTCACAC
AGGCTTTCCACCACAGGTGTTTATTCAGAGACATGAAAGCGCTCATCCA
ACAAAGACTCGTAAATGAAGTTTATAGCACCGTTTGTGGCCGAACTG
AGAAAACCCAAATGACCTTTAACCAGAGAAATATCTAAACAAATATCCAT
TCACATTAAATCAACCCATAAGAAGAACGGCTATGGGACGGGAACCGTA
TTGAAGAGGGTCAAAATACATACGAGCATCAAGAGACCTGCCAAAGG
ACACACTGACAGGTTCCATGGACTGAAACTCGAGAGGTGAAAACTCG
CCAGCAGTGACAGAGAGCAGGTCCGAGATCAACCTGATGTGGAGGAAATG
GAACCTCGTGCGTTGTGGCAGGACTATAAATGGAGCAGCCCTACGG
ACAAACAGTAGCCGGGCTCCTCTCTCCATCTCCCTGGGAGCCTGAGCC
TTGAGACGCTGGGGCAAGTGACAGGCTGCTGCTCAGCTGGGGCCCCGG
TGAAAACACGTGGCAGCTGGGGAAGAATCGTA

Contig 55 (735 bp)

TACTGCCTGTCTCTATGGACTTGACTCCTCTCGGGACTTCATGCGAGGGA
TCTTACAGAAATTTGTCTTTTGCATCTGGCTTGTTCAGTACGATCGTG
TCCCCAGGTCCATCCATGTTGACGCTGTGTGAGGATTTCTTCTCTTT?
CAAGGCTGAATAGTACTCCACTCTGCGGATGGACACGTTTGTATTATCC
ATACTAGTAAATCCATACTAATACTTGTTCAGTGAAGCCACAGCTTAT
GCTACCTTCCGTGGGCTCCTCCCTGCCCTGTCTACGCTTCTGTCTATA
GCCCCATCCCCCTCTCATCCAGGCCACGCTCTGTCCCTGGACACTGTG
CCAGAGGCCAACTGCCCTCTGACTGTGTCTCGCGTGACGGAGGACAAG
CCAGGCTCAGGGGTCCACGGGCTGGGGCCCGAGGCTCCCATGGCTGGT
GCCCTTCTCTGATCCAGAAATACAGTGGCAGCAGCAGCTTCCAGCTGC
CCACCTTCTGTCCGAGGCTGCTCGGGTGGGGCAGGTGGGCAGTGATG
TCACCTGCTGTAAACCCCTACCGTGGCTCATCCCTGTCCAGGAGGTAC
GGTGACCTTGGCAAACTTCTGAACACACACCTCCTCTGCTTAGAG
GCCGGGGGCTCCCGGGTGAAGTGGGGCACAGGCTGACCCAGCCTGTCT
TCTGTTCTGAAGGACATGATAAGTACTGCAACA

Contig 56 (500 bp)

AGGAAGAACAGGAAACAACGGGTTGAGGAGAAGAAACGGGTGTCTGGCA
GGGGACGTCGCAACGGTCCACGGGTGCTGCCGCGCTGCGGCTGGCGC
CAGAGGGGGCAGCTCCGCCCTCGGGCCCGGCCCTGCCGCTTGTGTGGC
TCGCGGCTGGGCTCTGCTTGGCTGGGTTACAGCTGGGTGCAGCCGAGGC
TGTGGTGGGTGCCCGGGGTGAGCCAGCCCGGCCACCCGGCCGCTCTC
GCCGGCTGGCCGGGCGAGCCCTCCTGCAGTCGAGGAGTCGCCCTGACGG
GCTGATTGGTCCACAGCCTCAGATGCAACACAGCCCACTGCTGGAGC
CAGCCAGCCCGGACACCTTGGTGGAGGAGGAAGGAGCAGCCTGGAGA
GCCGCGCCGATGATGCTGCGGGGAACCGGCTCCCGCGGGGGCGGCC
TGGCTCTGGCCAGGCTTGGCTTGAATGCTGAGCTGAGCGGTGGCCCTATA

Contig 57 (500 bp)

TGGCGTTGCAGTGGCTCTGGCGGAGGCGCGGCTACAGCTCCGATTGGA
CCCCAGGCTGGGAACCTCCATAAGCTGTGGGTGACGCCCTAAAAAGCAA
AAAACCCCAACATATATATATATATATATATATATATATATATATAT
CATAAAATAGAATTTACCTTCTTAATAATTTTCAGTGACAAATTCAGTGG
CACTAAGCACATTCATGCGGCCGTGTCACCTGCTCCAGAACTTTCCATCT
ACCCAAACGGACTCTCGGCCCATGGAACACGCCCTGCCCCCTCCCCG
GCCCTGCCCGCCAGCTCCTCCCTGTGTGTGGATCCGGCTCCTCCAGG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GACCCCGTGGCTGGGCTCACAGAGTGTGTGTCCTCTGTGACCGATCGTC
GTGTCCCGAGGGCCGTTCTGTGGCAGCTGCGTTATGACCGACTACCTTC
GAATGCTCAGTGACTGCCGTGCATTGGACACGCAGTCCGCTACCCCTTTTC
Contig 58 (550 bp)
TGCTTTCTGTGCCCCCTCCAGCTTGGGACCCAGCAGGGCAAGGGGTGT
ATAGGGCTTAAGGAGGCAGGGGGCGTCTCCTCCCGCTGGCTGCCAGAGC
ACCCCGAGCCCGCTGCCCTCGTCCATCTCCAGCTGTCTTTCTGT
GCCCTCCCTGTCCCGGGCGGGCCGACACTGGCTTCCACCTCCCCACCCA
ACTGGCGGCCGCTCCTCCTGCTGAGGCACCCGAGGTCCCGCTGTCTG
GGGACCACTGGCAGTGGGTCCACTGCTTTCTCAGCGTGGGCTTTGGA
GGGGGATCTGCACATACCATCCCTCAGGCCCGTGGGAGCCTGGGGA
CCATCCGGGACCCCTGTGGGACGGCCAGAGGACTGCCAGGAAGAGACCC
AGGGGACCAAGGCAGTCCAGGCCCTCTCAGCTTCAGGCCAGGGGAGCCCA
CCCCAGGTGGCAGGTGAAGCCAGGCCCAACCCACAAAATGCCCGCA
GGGAAGTAGGAGGACAGGAGGAGGGGAGGCCAGGCCCGGGCCGCTTTG
Contig 59 (800 bp)
TGAGGAGCGCAGGCCAGGCCCTGAGTGTGCCAGCTTACACCCCTGGCAG
CTTCGTCCCTCCTGGCCCTAACCCCACTCCTACCCAGCAGCAGGGGCTC
CCCGGTGGGGCTTGGTGGCGTCTGACTGGGGTTTGGAGTCAGGTCTGC
TCCAGGCTCAGCCCATCCCAAGGGTGCCCTGCAGCACTGCTGCCAC
CCCTAGCGCCCGCAGACCTTCGCCCTCCAGCCTGGATGTACCCACGGA
CCCTGAAAAGTGGGGCTGAGCAGGTGCCCTGGCTGGAGTCCCTGACT
GGGGCTGGCCAGGCTGCCCTGGAGGGCTGTGGGGCACAGCTGCCCA
GGGGCCCGTGGGCACTGGCTCTGGAGCTGACGACAGGCAGGCCCTCTCT
TCTGGCGGGGCCACACCTGCCCTGGGGTTTGGGGCAAGGCGGGCAGC
CCCATGTACGGCGGGGGCGAACCAGGTAATTACAGCCTGGCAGGCCGCT
CCCGAGCCCCAGCCCCGAGGGGCCCAACCCAGGCTGTGCCACCAAGA
CCTGGCATCCAGGGCCCAAGCAGCTCAAGGGCAGCTGCTACAGATCTTT
TTAAGTTGAGACAGAATCGACACATGACAAGTTCCTGGTTTATGGTACTT
CGCTGCCGGGGCCGCGCAGTCAGTTAGTGACCCAGCACACCCACACAGG
TACAAATGCTCTCTCAAAGAGGCCCTGAGAGAGCGCTGTCTTGGCT
CAGGGGTAATGAGCCCAATGGGTATCATGAGGTTGCGGGTTCCATCCCC
GGCTCGCCGCTTGGTTA
Contig 60 (500 bp)
GGCTCAGGAAGCGCAGGGGAGCGTGTGGGGCGACGGGAACCATGGGGT
CTGTCTTCCCGCTCTCCTCAAGCCCAACCGCTCTGTGCCCACTCCGAC
TCTGACGCCAGCATGCCGGCTAGAGCCCTGTGCACCCAGCTGGTGGCT
CTGGCTAAGGGCAGTCTGGCTGTGGACGCGTGTCCCTCCCGAGCAGCC
CAAGGGTCCCATCTGCCAGGCTGGTGGCTGAGGTCTGCCCTGTGTGGTCC
TTGCAAAAACCCGCCCTCTCTGCCCTTGGAGCGTGAGGGAGACGCGG
GCTGGCGGATGCCCTCGGGCACAGCCGCCCGCGGTGGCGCCCTGTCCAG
GAGGGGGCTCCGACGTGCCCTGACGGCCCTGGCCGGGCGGAGAGGGTGAG
GCCACCTCCTGGCCAGCTCCACCCAGCTGCCACGCCCTAGCCAGTGGC
CCGGGGCAAGTCAGCAGAGCCAGGCTTCCGACAGCAGAGGCTGTAGGC
Contig 61 (700 bp)
GATGAGGAAGCCGCTGCTCGTGTCTCGTCTTCTTGGCCTTGGCCTCGT
GCTGCTATGCTGCTTACCGCCCACTGAGACTCTGTGCGGCGGGAGCTG
GTGGACACCTCCAGTTTGTCTCGGGGACCGCGCTTCTACTTCAGTAA
GTAGCTCAGCGGGGACCGGGGGGGGGGACACAGCAGGTGCTCCATCG
GTGCTGCCCGGTACCTGTGCGGTCTTGGGATGGATGGTGTGGGGGA
CGGGGGCGGGGGCGGCCAAGGAGGACCTCTCCTCCGAGGGTCTGAGA
CTTCAGACCGGGGGCGCCCTGGCCGTGCGCATTGATTGGCACCTGCCATG
TGCCTGGCTGGGGCTCACACCCCTGACGTTCTTGCAGCGTGAACGAAA
CGGGAAACCAAGGACCGGGTGGCAGGGTGGGGAGGCAGACCGTGAGT
GGCAGGCGTGCAGGGGTTCTTTCGGGCGGGGTGCCAGGCAGGGCCCA
CAGGATGACAGCCTGTCCCTCCTGCTCTCTTGACCTGCCACAGCCA
GGGCTGCAGGCACTGACATTACCCATGGTATTGTGGTGCCTTGACGTCT
TGGCAGTGGCATTGGGTTATGGAAGTGGGAAATGAAAGTGGGAATA
AGATGGGGTTTAAAAACCAATTAAAGAAATAAAGGGCGCCCTGTGGGC
Contig 62 (300 bp)
TTTAAAAATTTGAGTCAGTGCAGATTTCGATCTATTCCGCATTACAG
CTCTCCTGTTCTACCTTGCTTAGTGCGGATCTTCTATAACCACCACAG
TGACGTTTCAAGGTACTTTATTGAATAATAAGAAAAAGTGACACAAT
CATGTAGTTAACTTTCTGTGCTTTGCCAGTTTGAAGGACCCCTTTT

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TTTCTTTTATAGGGCTTCGCCGACGGAAGTTCCCGGGCTAGGGGTTGAGT
CAGAGCTGCAGCTGCTGGCCTACAGCACAGCTCTGGCGGCGATGGATCC
Contig 63 (450 bp)
TCCTGGGCCACAGGCTGCAGCAGCTCACCTGGGGGCTGGGGTCTCGCTCT
GCCGATGGACCCATGAAGGCCGAGCCAGGTGGGGGCCGAGACGGCAGGG
CAAAGGGTCTGCACACACAGCGTCCCCCGACCCGGCTTCTCTGGGTCT
TGGGGGTTGGCGAGGCTTCTCTAGTCTGGGTTCCTGGGAACTTCA
AGAACTGGGAAGTCTTCCAGAAAGTTGGGGTGAGGGGAGGTACCCCCAA
GTGCTGCTCTTCTCCCCATCCCCACCCCTGTGTCATCGGCGAGACCCC
GGACCGCCCTCTCCCTGCCGAGGTGTGGGGTCCCCCCTCTGCCGGCCAG
GCTGGGCAGGGGTGAGCGCCCTCTCTGCACTCGGGACTCAGCCTGGG
GAAGCGGGGCCAGGAGTCTTGGCTGGACGGCAGTGACCTTCCACCG
Contig 64 (500 bp)
TGTGCAATCAACCCAGTGGCCACGGGGGTGACCTCGGCCGGTCAAGCC
GGCCGCTCTCCACGGAACCGGGCTTGGCCTGAGGCAGAAGGACCCAG
GACTCCATCCCTGCCCGGACTCTGCGGAGGGTGGGTCTGCACAGAGA
CCCTGTGGGGTCAAGCGGTGCGGGTGGGGTTGAGATGGGATGGTCAG
GGCGGGCCCCGGGGCTGCAGGAGGCTGGGTGAAGGAGGGGGCCAGCT
CAGACGCCCAAACTAGCTTGGGAGAGCTGCAGCCCCGGCCGCTCAAT
GGCGACAGCTTCCACAGAAAGGCAATCAAAATGAGAGACAAATTTGGG
CTTGAAGACTATACCCAGCCAGCTCTTCTGGGAGCCCAAGCTGCTCCCA
GGCCCTCATTGGGTATTAATTGGTTTCGTTTATAGATTTCCATGCTTA
TCAATGGCCACTGGGGGGTGGGCTGGATGCGGTCCAGGCTTTGTATG
Contig 65 (661 bp)
TCCACGACCTGCCCTCCAGGGCCACATCTGGCGACACCGTCGCAAGAG
TTGGACCGGCTGGTGTGGCCACAGCTCAGGCTTGTCTGGCCGCCAG
GCCGCTCCAGGCTCCAAGGAGCTCTGCTGCCCTCCGGAACCCAGCA
CCCCGGGGCCGCTTCCACACAGCTGTTTTCCAGGTCAAGGTACAG
CTAATTTGGGCTTAACTGGCAAGGAGGCTTATCTGGAGCAGGCTCCC
GGCCCTTGGGCTCTGCCCTGGTGGGAGGCTTCCAGAGGCTGTGTGT
TGGCGCTGACCTGCAGCCCTGAGCTTGAACCCGATAGGAGGGAGCCCC
ACCTGGGCTGGAGCCAGAGACCTCGTTCCCACTCCGAGGGTTCTC
ACAGTCCCCCCTGCCCTGGGGACCTGGAGCTCCAGCAGGTGAAAG
GTCCAGATGCCCTCTGACTAGAGGCTCTCCGCTGTCAGACATGCTCCCT
TCCCGCACCGAGGACGAGACCTCAGCAGCCCTGCGTGGCTGGGGTGGG
ACCCCAAGGCTCTCTGAGTGTCTTAATGGGAGCCGTGGGGCTCAA
CAGTGGGGTGGCACTTGGAGGGAGCCTCCCAAGCTGCCCAAGATG
GGCCCTGGACT

Contig 66 (500 bp)
TTTGTGGATGAATGAAATCATGAGAAAGTATTGGACCGCCCGTTCTGT
CCAGCTGCTTGGCAGCTGCTTTGTAAGATGACCTCTCACCTTCTCAGAG
GCCTGGCCGGCCGAGGTGGCAGTCACTGAGATGCCATGCTTGTGGC
ACGTGGGAGGCCCTGTCCACGGCGTGGGTGCTCTTGTCTTAATCAGG
GTCAGGGGGAGCAGCAGGTGCAGGGCACATGTGGGGCCGGGGCCGATGTC
TGGGGAGGGCGGAGGAGGGGGTGTGCGGAGGCGCTTGTGGGGTGCAGG
GGACAGACCCAGCGAGACCTCCCTGGCCAGGCACAGGACAGGTGATG
GGGGGGCCCTCCGGGGCTGTACAGAAAGCTCTCAGAGGAGGCCCTCC
CACGGTCTCTGGACCATCAAGGGACCGGGGGCGTGGGCTGGGGGTAC
ACCCAGCTGGCCGGCCAGCCGGGTGGGTGCGAGGCCGGGAGTTTAC
Contig 67 (550 bp)
GGGCAGGAGGGGCCCGGGCTGTTGGGAGGGTGGAGGTGGTGCAGGAGG
GTGTGAGGCAGGGCTCACTGAGCGTGGCGGCTGGCTGTGCTTAGAGTG
GTTAGCAGTGGCCCCACCTCCAGTGTGCTGTGTTCACTGTGCTGCTGG
CTCACAGGTGTGAAACTGAGACTCGGGTGTGTCATGAGCTTCCAGGATG
AGAATCAGCAGGCTTCCAGGCAGGGCTGTCTCGGGGCTCTGGGCTCTT
ACCAAGGAGGGGACACCCAGGGACAGCCCTGCTTGGGGGTGCGGGCTGG
CCAGGCTGGGTGGTCTTCTGTGGCTGGCAGCCCTTGGCAGTCAACCCC
TTACCTCAACTGCCCTCAGCTGAGACACGACCTCCCTGCAGAGCCCTG
TCCACCCAGACACTCACTCGCTTCTCCAGGAAGCTTCCAGGCTGCTCT
CGCCCTGGTCTCAGCAGGAGACAGAGAGAGGGTGGGGCCAGGAGCAGA
GGCAGGCAGCCAGAGGGGAAGCCAGGGGCCCTCACTACCCCTGGGGCC
Contig 68 (500 bp)
TTTGCAATCAGCTCGTACCCGGGATCCTTCCCGGGGCTCTGGGGTGGG

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FIGURE 6, CONTD.

GGAAATGGGGGTGAGAGGAGCTGTATCTGCCTGTCTACCTGCTCTCAC
AGGCTGGCCCTGGAGCCCTGGCCTCCTCTAGGGGCACATCAGGTTTGG
GGGAGGCCAGCCACCGTCCACCTCCAAGACCACAGCTGGGAGCCTGC
CCCCAAGCCTAGACCTAGTGGGGCTCCTGCCAGCCAGGCCCCACCTTC
ATGCTGCCACCCACCAAGGTGGGACAGTGCAGCCAGGACATCCAGCTTCT
GGAGCTGCCCGAGGCTCAGCACAGGCTGGTACCTAGGGAGCAGGTCAAC
CAGGGCCCGCTGGCGAGGCTGCGGGGACGGGGGTAGGGTGGGCAGCAA
AAGAACCTCTGAGCTGGGCCGGGGGGTGGTGGAGGCCGGGGCGCG
GGCTGTGTGCTGGCCCTGAGCCCGTGCAGACGCAGACCTGGTGGGT
Contig 69 (550 bp)
TGTGCTGCTGTGGCTGTGGTGTAGGCGCCAGCTGCAGCTCTGATTCCGA
TCCTTAGCCTGCGAACCTCCATATGCTGCTCTAAAAAGACAAACATAAAA
TAAATGGGTGCGCTGTTAATTTGAACACTCTGCCTCCTCCAGAGACGAG
GCCGAAACAGGCCTCTCTGAAGTCCACCTGGCAGGGAGGAGGAGGCCA
GCCCGTGGGGGGCAGAGAGAAGCCGATGTCCCAGACACACACGCACA
GGGACCGTGGCCCCGGCTGCCAGCCCCGGGGGGAGGGCAAGGCCAGAG
ACTCCAGCAGCCACAGGACCTTGGTGGCCACAGGACACAAACACAGGT
GACGGTGGGTGAGGCCTGGCCTTCCCCCCTGGGCACGAGCAGAGACA
CACAAGAGCCCCAGCGTGTGACCGCCAGCCCAAGGAGCTGGATGAAGC
TGGACACCGAGAGTCCACACTGTGTATTAGGCTGACGTGAAGTTTAAAG
ACAAGCGGGTGGCTCAGCGCTTGAAGGCCAGAACAGGCCGGGAGGGCAG
Contig 70 (1300 bp)
ATGTCAGGATAGTAACCTGGGGTGTGCTGAGTACAAATGCCAGATCCTTAA
CCACTGTGCCACAAGGGAACCTCTTACCTAGAAATCCTATACCCACTGCA
AATATATTTCAAAAAGGTAAAGTCTGAGCAGAAAAGCAAAAATGGGAT
AATTCATTTCTGGAAGACCTTCTCTTTAAAGGAAGTTTGTGGACGTGA
TGAAGGTAGAAACTCGGAGGCACACAAAGAAAGAAAGAAAGAGACAC
TGGAAACGGAGCAATAAAGGTAAATAAAGTTTCTCTCTTCTCATTT
TTTAATGTCTCAAAAGATAGCTGACCTCTAAAGTAAAAAATAGTGGAAA
TGTAGCATATGCTCTAGCGTAATTTAAAGTATAACTTATAGCAATGATA
GCCCAATAAAGGAGGAATTGAGATATACAGTTGCTGTGTTCCCATTTGT
GGCTCAGCAGTAATGAACCTGGCTAATATCCATGAGGATGCAGGTTCAAT
CCCTGGCCTCACTCAGTGGGTAAAGGATCCAGGTTGACGTGAGATGTG
ACGTATGTACAGACGTGGCTCGGATCTGGCATTCTGTGACTGTGGCTG
TGGTGTAGGCCAGCATCTGCACCTCCGATTTGACCCCTAGCCTGGGAACC
ACCATATGCTGCTGGTGTGGCCCTAACAGACACAAAATAAAATAAAATA
AAAGAGAGAGAGAAATATACCATTTGTAATTTCTCACATGACACAAAGAG
CAATGTGATATTTATTTGGTATATGGTATTGATTCAAGATGTATATCATA
ATATTGATTCAAGATGTATATATCTTTTCTAAAAAAGAGATTATACA
ATAAGGCAAGAGTGAAAAATAAGTGAATGCTAAAGAAATAGTTAATCCAA
AAGAGGCAGAAAATGGGGAAAAGACATATAACAGATGGAAACAAATAAAA
AAGAGCTAATGAGATTGTAATAATTTAATCCAAACATACAGATAATCCCAT
TAAATTTAAACACTCTCAACACATTGATTAAAGAAATTTGCAAAATGAA
TAAACAAAGCAAGACCCCAACTAGATGCAGACTATGAAAAACCCACTTCAT
ATAAGACATGGGTAGGTTTAGAGCAGATGATGGGAAACCATGTACAG
CAACATTGTCAAAATAAAGCTGGTGTGGCTGTATTCTATCTCAGACACA
GCAGACTTCAGAACAGAAACACTGCAAGGATGAAAGAGATACTGCATA
ATGATAAAGGGATCAATTTCCAAAGTGCAGGCTCCAACACACAGAGTTT
Contig 71 (500 bp)
ATGACCTCATACTGAATCGAGCTCGGTATCAGGGGATCTCTCAGCTGGGG
GGGAGGGCAATGGGGCATTTGTCTGAGGATGCCCCAGGGCAGGCCATTG
GCTGGTTTGGTGCCCATGCCCCCCCACACCCCGGCACTGCCCTGCTG
AGCCTGGGACCCCTCTGGGAGTTAGGGATTGGGGGTGGGAACAGGCTT
TGCAGTAATTCAGCCCCAGGGCCCTTCCCTCCCCGCTCAGGACCCC
CAGCCCCGCCCCACAGTCTCCACTGTGACAGCCTCACCCCTTGGGTCA
AGTCTGTCTCTCCGGCCCCCGCTGGGCAGTGGAGCCAGCTAGGTGAGA
GGCACAGGCCACTAGGGCGGTGGGCACTGCTGAGGACAGAGGGGCTGGG
TGGCCTTGGACGAGGCCACGCGAGCTGAGACAGTGAGCCAGGCTCCAGG
CTTCCAGGGAGGGTCCCTGAATGTCCACTTCTTGTGACATCGGGTGAC
Contig 72 (550 bp)
AAGTCCATTAGGGAAGGATTTGTGCAACACAGAGACAGGTGCAGGGCT
GGGCCAGCTGCTGGGCTGGGGGCTCCTCAAGGCGCCGTAAACCCCTCCC
TGCCAGCCGCTGCCGCCAAGGTCTGCTGCCACCCGGCCGGGCTGCTG
TGTTCCCGGCTGTGCTGCGAACCCGACTCCCGTTACCCCTGAGCAC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TGCTGGAGCCGGCTGCCAGGCGGACGGGCCCTCAGGGCTGGGCTGG
CTCTTGGCTGTGTTTCATTTCTGAGCAGGTCTCTCAGTGGGGGGGGC
CTTGGGTGAAGCAGGCATGTGCACCACTGGGGCCCTGTCCCACTGGGCA
TCCTGGGCGCTTGTCTGGCCCCAAACCCAGGCCGTGTGCATCATAACC
TTCACCTGAGCCCCAGCCGAACCCCGACATGTGCTGGGGGACCTGGG
CACAGGGGTGAGGGAGCAGTGGCCTTGGTGGAAAGCCAGCCTTGGCACCT
GGGGAGGGGGTGCATCTGGCATGCTCTGCTGTAACCAAGCCAGGGCAGG
Contig 73 (950 bp)
GACGTGCAGTAGCCATGACCTCTACGGCCCCACTGACCAGCCCGTGTCC
TTGTCCCGAGACCGACCCCTAAGCAATAGGATGCAGCAGAAGTGACAGAA
CGGCCTCCGCGATGAGGTGCGAGAGGGCTCTGGCTCTGACTCAGGCCCT
CATCCCTCGCTCTCTGGAGCAGGGCCAGGTAGGGGCCCCAGAGACGC
CTAGAGGAGGTGACGGGCGAGCCAGCCGCCCCAGGGAAGGCTGGGGAC
ACCAGGGAACAGAACGGCACAGGCTCTGGCACAGTCTCCAGGAGCCCC
CTGGTGGCACAGAAATCTGACCGGCCAGTGGAGGGGGCTGGGGCGGG
CTCGGGGAGGAGGACTGGGTGAGGCCGTCTGACTCTGGCTGAGCGCCG
CATACTTGTGCTGCTGCCACGATGCGGGCCAGGCTTCCGCACGGACCC
AGGCTCACATTGCGCTACATGCCACTGTGTGGGAGTTTGGGATGGTGTG
CCCGCTGGGCCCGGGGTCAGGGCACGCTTCCAGAGGAGCGGTTCAG
AAGGCCAGGTGGAGAGGCGATAGGAGGGCTCCAGGGGGCTTCCAGGCC
ACCTGCGAGGACCTCTCTGGGGGGAAGGGAGCGGAGGAGACAGCCGGGT
CCCTTAGGCCAAGGCTGAGTTGTGACCGCAGGGAGAGAGAGAAGGAGCA
CCCACAGCAGGGCAGGGGCTGCGGGAGGCTGTGCTGGGTGGCCGGGTGGT
GGGTCTGGGGGCCAGGACCGTGGGAGGCCCTCGAGGGGGGAGCAGGCACGG
GAGGGGCCCTTGGACGGCAGAGTCCCTGCTCCAGCTGCCGCCCGACCCC
AGGTCCACCTTCACTTTCACAGCCTGGCCCCCGGCCGTCTGACCGGCCCT
GCCATGCAAGTGTAGCGGGCAGTGAAGGCCAGGCTCCGGCGTCCCAA
Contig 74 (450 bp)
GCAGGCTGGCAGCAGGAAATGATCCAGAAAGTGCCACCTCAGCCCCCA
GCCATCTGCCACCCACCTGGAGGCCCTCAGGGGCCGGGGCGCCGGGGGCA
GGCGCTATAAAGCCGGCCGGGCCAGCCGCCCCAGCCCTCTGGGACAG
CTCGCTTCCAGGCCCGCGGCAAGCAGGTCTGTCCCTGGGCTCCCGTC
AGCTGGGTCTGGGCTGTCTGCTGGGGCCAGGGCATCTCGGAGGAGGAC
GTGGGCTCTCTCTCGGAGCCCTTGGGGGTGAGGCTGGTGGGGGCTGCA
GGTGGCCCTGGGCTGGGCTCAACGCCGCCGCTCCGCGAGGTCTCTACCC
CCCCCATGGGCCCTGTGGACCGCCCTCTGCCCCAGGCTGGGCCCTTGC
TGGCCCTCTGGAGCACCCGCCCGCCCGGCCCAAAGCCTTTCATGAACA
Contig 75 (1363 bp)
CCTCCAGCTGGGCCCGGACAGGACCGTGGCCCTCAGGGGACACACGGG
GGGCCACAGTGGCCTCTCTGCTCCAGGCTCTGCTCCCGCTGGGGCCCC
CTGGGCCGCCCGCCATGGCCAGGGCAAATCCAGTGCGGCTGCCCGTC
TGGGCAAGAGGCGCCAGGCCCGCGTGGTCTTAGCAGGCACTGGCGGA
TGCCGNTAACTAACCTTTCTTCCGAGGAGTCCGAATCTGCTGACCA
CGGGCCCTAAAAATCGCTCTGGCCCGCAGAGGATCCCCGAACAGCGGG
TAGGTACACTCCCTTGGGGCGCAGCCATCGCACCATCCGCTTCCAGGAG
GTCCCGTCTGCTCTCTGCTGCCGGGCCGCACTCGGCAGGCACGTGCCCTC
GTGTCCTCCAGTCTGTCAACCGTCCCGTCTGTACGATCCCAAGTCCCA
CGCGCGGGCAGCTCTTCCACACCCCGCAGGCCCGCGGAGCTGCCTGGGC
ACCCAGATCGCCCTGACGCCCTTGTCTCTAATTCTGCTGAAATACACAT
AACGTCTCTTGAACGTTTGTCCATTTTACGGGGACAATTCTGTGGCGG
TAGGTACACTCCCTTGGGGCGCAGCCATCGCACCATCCGCTTCCAGGAG
GTCCCGTCTGCTCCAGATGGACACTGTCCCACTGATCCCTAATTCCCTGT
CCCCCCCAGCCCTGCCCTTCTGTCTGTGGCCCTGGCGCCTCCAGGGA
GCCCTTGTGCGTGGGATCAGAAAACGTGTGTCCTTTGCGTCCGGTGTGT
GTCTCTGAGCATCCGGAGCTTGGGGTGTCTCCACGCTGCGCCTGTGTAG
GACGTCTTCCCTTTTGGGCTGCGCATGCTCCCGTGGGGCTGCCCCA
CACTGCGCGTGTTCGCTCATCCATCCACTAAGGCTGAGTTACTTTTGGCG
GTTGTGAATACTGCTGTGTGAACACGGCGTGCAATACCTGCTGGAGGC
CATGCTCTTAGGCCCTCTCGGGGGGCACACCCAGAGCGGATATGCTCAATA
AGGTAATTTGTGTTTAGCTTTTGGGGAACCATCAGGCTGGTCTCCAGA
GTGACGGAGCATGCGTCGCAATTCACAGGAATGGTGTCTGAGGCTTTGAGG
TCTCCACCACTCGCTTCTATTTCTGTGCGTCACAGCCGTCCGAACGGC
TGGGTGGTGCCTCTGTGTGGCTTCAATGTGCTTTTCTTTCTTCTGGCTAT
GAGGTTGAGCGTTTTTATGTACTTGTGGCCATTGCGAGGGTTTTTGGG
GTTCTTTTCTTTTGGCTTTGGGGACGGCGCCAGAGCGTATAGAAGT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

TCCCTGGCTGGGACTGAATCAGAGCTGCAGCTGCCAGCCTAGCCCCACAG
CCGCAGCAACGCA
Contig 76 (500 bp)
TCATGCCATCGCCACCGCCCCACCCGACGTTTCAAACACCAGAACCA
CCCCCGGGCGGCAGAGAGAGGACCGGAAGGAGAGACAGCCTGGTCCCAA
GGCCTCGCCCGGTCTGTGTCTCCGAGCGACATTTCTTTCTGTTCCCTC
CTCCGCGGTCCAAGTTTACCCATCAGAGGCGCATTTGTTTCATCATCTG
AAAAAAAATCTCTGTCTCTTAATAAAACACAAGAAAAAGTAGCCTTCGA
AAGAAAGCAGATGAATGATATGTCTGGCGACAGTGTGGCGGCCTCTGA
GCCGTGGTGGAGGTGGGAGCCAGCGGAGCCCTGACCGATCACGTGACC
CACGTCTCTCTGCACAGCTGGCTGCACCTGCACCGGTGACACAGGGAC
CCAGCCTCCTGCCAGCAGGTACCCACCCCGTCCGTCTCTCTGGAAGG
GGCAGCGTTGCCCTTCTGAGGGTGGGCTGCTCTGAGGGGCTCTTTGGCC
Contig 77 (626 bp)
GCCATGGGCTGCGGCGGTTACGCGGCTTGCCGGCTGCCCTGGAAGTCCC
ACAGGACCAAGGGAGGGGACGTACGACAGGGGCCCCGGGACGGACGG
TGCCGCCAGCGCCCCGGCCCCCGCTCCAGACAGGACGCCCGTCCACC
TTGCGGGGACAGCCAGCCTCGTGGCCTCGAGCAGAAAGTGAGAGTGGG
GTGCACAGGGGCCCCCGGGGAGGAGGGGACAGCGGGGTGAGCGGG
TGGGGCGTGTCTGGGACCCAGCCCTGGCCTCTTGGCGCTCCTCCTCCCG
TCTTAAACCGGCCAGCCTCTTGGGCTCGACCAAGGCTGTTTGGAA
AATAGGTGAGCCGTGGCCTGACCCGAAGGCCAGCGGGACCCGAGTGGC
GTCCCAATGGATCAGCAGGCGCTGGGAGCCTGCGGCCCGGGACCCG
GAGACACAGGTGGGAATGGGAGGAGGAGGAAGACGGGAGAGAGGAG
TGAGGACACAGAGAAACACGCCCTCCTCTCTTCCGCTCTCGCCCTCGC
CTCCGACAGCTCCGACTCGGTGCAAGGAAAGGCCACAGCCAGCCCGC
CGCCACCGGG
Contig 78 (500 bp)
TACTCGGGTTTGTACCCTGAGCCACAAAGGGAGCTCCTAAAAATAATA
ATTTCTTAAAGCCAATGACATGGAGAGCAGTTAGCGTGGAGGCTGGTGG
GTGGTGGGGCGCGGAGGCGCCCTGAAGGTCTTGAAGTGGCAGCCCTTGGC
CGGGGAGGTGGGTGGGCGAGGGGTGTTGAGAAGGGGAGGGCCTCGTGG
GGGAGGAAGGAAGCCAGTGGCTCCAGTCCCTGACCTTGTGCTCTT
GAGCCTGGTTCTCCCAAAATTTGTCTGTGTCTCCTTCACTTACCGGAAG
CTTGGGGCCCGTTGCCAGGGAGACAGATGGGCTGGTGACACCAAAATGA
GCCACAGGAGGGGGGCACTGACTTAGCCAGCGGTCACATCAAGAAGC
AAACAGGCCCCCGCTGCTGTAAAGGCAGCTTGGGCTGGGGTCCGGGAG
CACCCCTGGGCTGGGAAAGGGGTCTCTCAGGCCCGGGGAGGATG
Contig 79 (427 bp)
TCTATTGCGCGTGGCGGAAGAGGCTAACCGTACATTGACCGGCATCTG
GCGATGTATCACTTCTTCCAACCGAACTTCCGGCMAAATTGCTGCG
TGAAAACGTTGCGGATAGCCGAATCTTACCTACCGTAATACAGTCATTG
ATGCACTGTATGGGTGGGTGACCAAGGTGATGAGCAGCGACAAGCTGCGT
TCAGAACTGGCGGCAAAATACCCGTTTATCGACCCCGATAAAAAGATGAT
TCTGGTGACCGGTACAGGGCTGAGAGTTTCGGTCTGGCTTTGAAGAAA
TCTGCCACGCGTGGCAGACATGCCACCACGACAGGACATCCAGATT
GTCTATCCGGTGCATCTCAACCCGAAGCTCAGAGAACCGGTCAATCGCAT
TCTGGGCACTGTAAAAATGTCATTCT
Contig 80 (650 bp)
GGCGTTGCCGTGAGCTGTGGTGGGGTCACAGATGGGGCTCAGATCCCGC
GTGGCTGTGGCTCTGGCTAGGCCGCTGGCTGCAGTCCGATTCGACCCC
TGGCCTGGGAGCCTCCATATGCTGCGGGAGCAGCCCTAAAAAAGGAGG
AAAAAAGGAAGAAAGAGAAAGAAAGAAAGAAAGAAAGTCAAAAG
GAGCTCCCTGAGCGATGTCTGTCTACGAGCAGGTCCCTGGGAGCCTGAG
GCAGGGTGAGCCTGGACCCCTGAGGGCCACTCCAGACTCAGTGTCTCAC
TGGCCAAAGTCTTTGGGACCGGCTGGGGGCGCGCGAGGCTAAGGAGGA
GGTCAGAGGAGGGGCTTCAAGCTGCAGGGCCAGCGCAGCTCTGGGCCCG
GGCGGGGGGAGATGGCTGAGGGCTTGGGGGGCTGGAGGGTGGGGG
GCTTCTGGAGTGGGAAGACGGGAAGCCAGGTGAGAGGAGAGCGAGG
GCTGAAGCTCCTGGAAGGCGCTGGCTACCCCAAGCTGGCCCGCCCGCTG
CCACATTCAACAGCCACCCGCTGTGGTCTTGGCAGGGTCTGGCAGAA
AAGCCCCAAGGGCCCAAGCCTGGCCCTTGGGCTTAAAGAGCCAAGCCCC
Contig 81 (550 bp)
TTAACCACGGAGCAAGGCTGGGGATCGAACCTGTAACTCTGGGCTCCT

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

CGTCGGATTCTGTTAACCCTGCGCCACGACGGGGACCCCCAGGGCTGGC
GTTTCCCTCTGTGTGCACACAGTGGACCTGAGCCAAACAGCAGGGCCTTC
ACCACACGGCGCAAGAGTCGGCAGCAAGAGAGCAGTGTCTCATGGCTCA
CTTTCTCCCCCTTCCCCGGAGTGGTGACAAAACCCCGCCGACCGGACT
CGGTTAGACAAGGCGGTGCCAGTGCCCCGCTGTACCCGACGGCAC
GGCGCTCTCCTTTCTTCTCGGGGCTCCACCAGTGTCTCAGTTTCCGC
ATGAGAGTACCGCGCTGGCGGGGTGGTGGCTCTGGGGTGGGGGGCGGTG
AGGGCAGGGCTGGGTGGGGGAGGAGGTCTTGGCCATTACGCGGGGGG
CAGACTCCACATCACAGCTCTCTGTGCCTTGTGGCTGCCTGACACCATG
GACTTCAAACAGGAACAGCGGTGGAGGCATTGCAGCCAGGGCCCGGT
Contig 82 (550 bp)
TGACACCTCCAGGCAGGAGGTGCAGGCTGGGGTCCCAGGTAATGGTGTG
CTGGCCTGTGGGGCTGGGCTCAGCTCTTAGGATGGTGGGTGGGCGCGG
ACCCAGCAAGGACAGGGTGATGGCAGGTCTGGGCTCAGCAAATGAGTGC
CCAGGTTGTGGGGTGGGCACTTGGGGCTCAGGGGAAGCTCATCAGCTTG
GAGAGGGACGGGGAGGGAGGGGGCTTGGCCAGTGGCCAGATGCCTG
GATGTGAGCACTCACGTGCCCCGGGTCCACCTCCCTCCAGTGGCATCT
GGGCAGGAGGTCCGATGCTGTCCCTGGGACCCGCTGTCTGAAATGAG
GTTCACTTGGTGCTTCCCCAGAGATGCTCGGTCCGGAAGCTGACGAGGC
AGGAGTGCACAAGGGTCTGGGGAATGGAGCAGAGTGGGCTGGGGCACA
GAGGCTGCCCCAGCCTGGGAAGATGGGAGCTTTGACGGGTACCCCGC
CAGCTTGTGGGGCCCTGGATACCAAGGTTGAAGAGGCTGAAGAGCGA
Contig 83 (984 bp)
CTGAGCCAGCTATGTAGATTAGACCCGGTCCGTCCCAAATTTCTTCTCA
AAGCTGTCCCGAGATGAGAGATGAGGTTTTCGTGCTCTGTCTCTCCTCG
CTTCCCTTGGGATGTGCCCTAGGGTGGGAGAGGGTGTGTCCAGGGCTCA
GCAGGCGGTCCCATCTTCCCGAGACGGGAGAGATCCCTCTTCTCGGCG
CTGTCTCCACGGCCCCACAGACACCCCCCCCCGGCATGGCACCCAT
GCACCTGCCATCGTGCCAGTAGGGGATGGGTTTGGCGAGACTGGAGATG
GCTGTAGCCAGTGAGACATGCCCTGCCAGTAGCTGACCCCTGGGTGT
GCTCTGTGAGATCTGGGACCCACAGCACCTAGGGATCATCTTGCCA
GCCTCTTGGGAGCTCTCAGAAATGGGGGCCCCAGAAGGCTGGCAAAG
GTGATGGGAGCGTGGGAAGTCTGGCGGTTGGCGGGTGGGTGGGGGCA
TGCGGGCTGGTGGGGGTGTCTCCGGGTGGGAAGTGGTCCAGCAAGGT
TTTGGACACAAAGTCAGGAGGAAGGAGTGACGAGGAGACTTGCAGAATTA
CAGGTAGAATCAGGAACCCACATCGACGCCAATTGATCTATCCCCCTT
TGATTGTTTTCTCCTGGGGCTTTTTTCNTTTTTTTTTTTTTTTTTT
TTAATCCCTCTTAGCTTTTACGCGCTCAACACCAATTAACGTACTC
CCACCCACGTAACAGGGGGGCGGTGACCCGAGGACGAGGAGCACAG
AAGCCACCATCCGTACCTTGGCGGCACAGCCGCTGTCTGCCCTCCGC
CCATTTATCGCCCTTGAATTGATTTTGTGTTGCTGTCCCTGTGCTT
GGGTAGAGTGGAAAAGGGAACCTCTGTGGGGTGCCAGCCACTGGGCCCC
CCAAAGATTTCAGGGGAATGAAACGGCTGCCGCC
Contig 84 (550 bp)
TGCCCCTGACAACCTGCCCTGTTAGCCACACTCGCGACTAATAAGGCGA
GAGGTACGCGGGCAGCCCCACGGGAGAAAGTGCTCCGTGCCCCACC
CCTGGCTCTGATGGCCAGCCTGGCACCCAGGTGGCTCGGCTTCTCT
ACCTCCAAGTCCAGGCGCATGTCCAAGCACCAGCAGAAGCTTCTCAGG
GTTGGTGCCTGCTCAGGGCAGAAAGCAGGGGTGAGGCTCCCAAGGGGCC
ACTGGCACCAATGCCCCAGGCAGCCAGCGAAGGGGACAGCCACCCC
CAGCCCGGGGACGAGGCCCTGAGGGGACATGGGGAACCCAGAGCAGGGCC
AAGGGAGCAGAGCCCTCTCCGGGACTTGAAATCTTCCCGGGGGGCC
CAGGGAGCTGGGTCTGCAGAGGGCACTTCAAATACGGCCACCCCA
AATTGCCACGTGGGCCACAGAGCAAGGAGTGCCTGCCAAAGTGGCCTGGC
TTCAGCGCAGGAAGTTCCCTCTCGGGCTCCCTCTATAGGCACAGG
Contig 85 (500 bp)
TGAGCCAGGGCCTGGCCAGCTAAGCCCTGGAGCCCTCCCGGCTGTTT
CTGCCTCCCATGCTGGCGGAGCTCGGCTTACTGAGCGGGGCGCAGGCCA
GTGTGCGTGTGAGGTAGATTCCACTCAGCTGAGGTTGAGGTGGGCAGG
GGGCGCAGACCTCAGGCCAGCTCTGGCCGGCCAGGTCCCTGAAGCTCC
CCCGGCTGGCTCCCGCTCCCTGCTCTGGCTTGTCTGGCCCTTGCTT
GACAAGCTTCTGTGCTCTGCTGTCAGGAGAGACACTGGCTCCCGGCTC
TCGATGAGGACGGGCTTTCTGCACAGTCTGCCCCAGAATGTTTGG
GGGCCAGCAGCTGAGCCAGCACGCTCTCCCTGCCCTGGCTGGACAC

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GAATCCCGGCATCGAGGCGGGAAGGGGATGGAGGGATGGGGCTACCCA
CCCCTGCTCCCCACCCAGAATAGCTGGGCGGCCCATGGGAGGCGGCC
Contig 86 (913 bp)
CTGTTTTCACGTCTTCTGAGGACACACCAGAAGAGGGCTGCAGGCGCC
CATGGTGAATCCATGTGTTCACTGCTGAGGCTCTGCAGACCGTCTCCCG
CAGCAGCGCGCACCCGTTTCCATGCCACCAACAGCGTGCAGGCGCGACTG
TCCCCACGGCTGTGCAACTGTTTGAATCTGAGTTATATAAGCAACAGAC
GCTCCTTCAAACACACTCAGTGCACACGTGCGCACAGGCGCACAGACAC
ACACACGGAGTAATAGGCTTCCCCCCTCCCTGAGCCAGAGGGGCT
GGGGCCCTGGAGCCTGTGCTTTAGGGCTTTTAGGAAAGCTGGTGCTCC
CAGAGGGGCGCCCGAGCGTTGGCTTCCCAAGTCCCCACCAACCTCGA
CAGACTCAACGTTGGTTCTTCTGCTTTTGGCCAAAGGATGGGCGCG
AGGTGGCCCTGCTGAGGTTTCAAGCCAGCGCCCGAGGACCCCTTCTCT
CCCGGTCGCCGCGCACTTCAAGGACAGCGGCTTCCCCACGTTGTCC
CCTGGGTGTCTGCTTTTCTAATGAGACGAGGCGAGGTGCACCTGTCC
TGGGGTGAATTCCTTCTGCAGGAACCTGCTTCCCGCGCGCTGGTCTGT
CTGTCTCTCGTTGTGGAACCTCTCGTCAACAGAAAGGTTGGTCTGTAC
GTCCCTCTTCCCTCCGTGGCTTTGAGTCTGGGCTTGTGCGGGAAC
TGCCCCAAAGAGGGGAGTGACCCCAAGAGGAGAGCTAGCTCCTGTGG
CGACAGCACCGGGGCGCCAGATTATGGGGTTCACGCTCACAGTCGA
TGACGCTGCTTTGGACGAGGCGCTCAAGGGAAGCTTGTTCCTGCCA
CGAGCCACAGGCA

Contig 87 (650 bp)
TCCACACCTGTGGAGCCGCTGCCTGCTGATGCCCTCTGCCAGCTGATG
GTCAAGTGCCCAAGACTTGGGGCTCAGTCCAAACAGGGGCCCCACAGGTGCT
GCACCTGGGCAAGGAGGCTGTGCGCAGGGGCTCAGGTGTCCAGGCTCG
CTGGGACCGAAGCGCACTGGGTCTGGACTCCGGCTTCCCCAGGGCTG
CTCGGGCCACCTGGAAATGAAGCCCCACCTGGCTCATAGGTTCCACGTG
AGGGCCCTGAGGCCACCAAGCCACCAACCACTCAGTTAAGGAGGGGAG
CTTGGGGCTGCTAAGCTCCAAGCGGAAGCGGCGCACTCAGCACTGCTG
CTCTGCCAGCCAGCGCCCTGCTGACGTCCCAACAGGCGCAGGGAC
CCTGTCCACAGATGCTGGGCTTCCAGTCTCTGCTCCTGGAGGCGCT
GGGCACTGTGTGGGCACACAGCCCGACCCGCTGTAAGGAAGGGAAGG
CCCCATCCTCAAAAAGCGTGGGCGAGTGGGCTGATGGTCTCCGAG
GAGGTCTCTTGGGACCCCTTGTCTCTCGGGCTCGCCAGGAGCGGCC
AGGTCTGCCCTGGATTAACTCTGCCCCGATGTCATTTCAAACTGGCTT
Contig 88 (700 bp)
TGGGGCCCTTTGGGCGGAGCGGCCAGTCTGCTGGGCGGGGAGCAGGG
GCTCTCTGTCGCGAGGGAGGGGCTGGTCTCAGGGGAGGAGAGGCA
GGTCTCACCTGAAAGGATCTGCTTCTCCTCAGGCTCTGGGATGCTGG
GCAGAGAAACAGAGGAAAGGCCCAACTTGTGGCTGGTGGGATGGGG
CGGGGGTCTGCTCCCGGCACACCCCAACCCCACTTAGTGGCCAA
AGTGGGTGTATGATGGCCACTGACCTCACGGGGGCGCAGGAGCAACAA
AATTCAGCCACTCTTGGGGGAAGGACACTTGTGGCTGAGTCTTAGGGG
CTGAGTTTGGGGGGGACCCCACTCTCCCCCAGTATGAGACACCTG
CCCACTCTCCAGCTGCTCCCCAAACCACTGCTTCTGGAGGGGATCT
CCCCGCTGCCCCGAGCGCTGCTCTGACCATGTCCCTCCCACT
CCCCCTGCGAGGCGCAGGCTCCAGGGAGCAGAGCCAGGCCCCACCTA
GACTGAGCTGGGGACCGAGACCCCAAGTCGCCACCCGCTCTGCGTTAG
AGAGGGGTTCCGGGGGACCCCTGGGGCGCACTGGGGGCGGGAAGGA
GAGCCCTGGGCGTTCTGGGAAAGTCTGGGAGGAGGGAGGGGTTTGC
Contig 89 (1400 bp)
GCACACCGGAGAACAGAGGGAGGGTCTTACCACTCTCAGGGTTTTTT
TGGGGATTCTTTGAATTCCTTATGTTTCGAGGCTTCTGTTCTCTC
CAATCCCCCTTCTGAACCCCCCAAAATGGGTTCAAGCCCCACCCAG
CCAGAGGAAACCAATTGGGGGATGGGGGAGGGGCGCAGCAAAAGCC
TTGGGCCCCAGCCCCCTGGCTTTGGCTCTGGCTGCCAGGTAGGGG
AGGGACGCGGTGACCTCCGGGGGCTGGCCACGACTCTGCCCCACCCC
CAGGGCAGAGCTGCACAGGAGGGGAGGCTCCAGGAATGAGGCCATCA
AAGGGACAGGTGAGGCCACGAGCGTGGGACCTGGAAGTGTATTAGGGCT
GGGGGACGAGGCTGCGGCTGCGGGCTCCGTGGTCAAGAGGCTCTGCC
CACTGAGCAGCTCCCACTGGCACAGGCTCTCTGGGGTCCGGCTG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

GTCTCCGGCAGGGGTGGGCTCTGAACGTCCAGCTCCGCAGACAAATCAGA
 TTCCCCGAGCCCTGAGAAAGCCCCCTCCCCAGCCCGTCTCCCCACCTG
 TCGGTGGACAGAGTGACCCCTGCTGACCCCTGCCCGGGCTCCCGCAGGA
 GATGTGAGAGAGTAAGAGGCGGTACAGGACGGCCGGGGCGGGCCGGGCGA
 GGTGACGGTGTGTGGGTGTGAGGCTGGGCACAGGCTGGCACAGCCTCCCT
 GGGCCAGTCCCTTGGGCACCTCTGGGCACCTCGGTGTGCTGCCTCCTGA
 AGGGATCCACCTCCAGCCACCTCCTCTCGGGCCAGCCCCACCCACCC
 CCGAGCTACAGATGCTGCGCATTGCCCCAAGTGTCTGGACCTGGAG
 CCAGGCAGCCACCCGCTCAGCCTGGCCAGACCCAGCGTTGCCCTTCAGC
 CCTCTCTCTCCCGCGGGTCTCGCGCTCGTCTCCTCAGGTGGAAAGC
 CCTTCCCACTGCGCATCTTGCTGCGCCAGGATACACGGCTCAACTCA
 AGGCTCACTCTCGCCCTCTCCAAGGCTCTGTCCAGGCCCTCTCTGAC
 CTGGCACCACTGCGCCTCTCTGGCAGCCCAAGCAACCCCTGCCACAG
 TCCACGACAGTCTCTTCTGGCTCTGCCCCAGGATGCTTCTAGAACTGG
 GGGGGGGTCTTCCAGCCACGCGAGCATCCACTGGGCCCTGGGCTCCTC
 CCCCAGGTGCCCTCAGAGCTTGACAGTGGTGCAGACGGCTCTGTCCGA
 ACCCATGCTCCTCGCCCTTGGACCTGGTGAGATGTTGCAGGTCAATTG
 GCTGCACCAAAAGAGTGGCCCTCAGGGTCCCCCTGCGCCCTCCATC

Contig 90 (350 bp)

GTACTGTAGGGCCTCATTGGAATAGCCTACTAGGTCACAGCTGATCCACA
 CCTTAGGCCATCACAACCTCCAGAGGTAGTGCCGCTCCTGTCTGTGAAC
 AAGACGGTAGTGACTGCTGTGAGAGCTCAGATCTGGTGGGTCACTGACCG
 AGTGTGGAACCTGGGGGAAGGCTGTGGGTGTCCCGGCTGGGTGGCCA
 TGTCTGTGCCCCCTTCTATCCCTTGGACGAGGCTGGTCACTCGGCTCT
 AGAGCCCCAAGCCCCAGCTGCTGTCCAACCCCCAAGCCTGAGCCTCAT
 CAGACCCACCCCATCGCCATGGCTACGAGGACACACCGCTCTCCAC
 CCCCACGAGCGCCCACTCCCGAGGTTCCAAGCTTGA

Contig 91 (1464 bp)

TCCAGGACCTGATGCAGCAGCCACGTCCCGAGGCCCTCCACGAGGCC
 CTGTGTGACAGCGCTAGGGAAGGGGACCAGGGAGATGCTGAGAAGGGG
 CCTTCCGAGGGGGCAGGTGGGACTGACTGTGACCCAACTCCCCACCCC
 CCTCTCCCGCTCCAGAGGGTGCCAGCCTGGAAGCTGGCAAAGTCCAATCC
 ACAGGTGGGCTCAGGTGGGAGGCTGGTGGCCCCACCTGGTGGGGCCC
 AAGCTGCCCTTGGGCGGGTGGGGGCTGCTCCAGCAGGGTCCCATCCAG
 CTCTCTCTGGGAGACTCACAGTTCTGGGAGAAGGGTCTGACTGCACC
 GCAGCGCCCGCCCCCTCCCAAGACTCACCAAGTTCTCTCTGATCGG
 TGAAGTGTCTCCGATTTGCCAGGCTGGGCATCTGCCAGAGGATACGT
 CCAAGGCGAGGCAAGCCGGGCCGTCCCGGAGCTCCCAAGGCGC
 TGAGGGCTGGGCTGGATCTCGGGGGGTGGAGGGGAGGACTCAGAAGGTG
 CAGCGGGTGGAGCGAGGCTGAGCCAAGGTGCACGCGAGGGCCAGAGAAG
 GCCGAGGCGGGCAGGAGGAGAGCGCCAGCCTGGAGGGGGTGGGTGCC
 CTGGGAGGCTTGGGGCTCAAGAAGAAGAGAGTGTGTGTCAGGGGGCTG
 TCCAAGCTGCCGGGAGGCTGCTGCCACCTCCAGGAGCAAGCAGGG
 AGGCTGCAGCTGGCCCGGCCGCGCTCTCCAGGACACCGGTGGCCAG
 GCCTCAACGCTCCTCCCAAGCCAGGAGACCCAGGGCACCGGTCCATT
 TACCGGGGCTCCGGGTCCGTTTGCTGCGCCCTGGGATGGACTGTGGGG
 GCGGGCGCTGTCTGGGAGGAGGGAGGTGTCTGAGGCTGGACACCTTGA
 AGGAGGTGAGAGTGACAGGTCCGTGCGCAGGAGCCTTCGGCTCTGGATT
 CTGGCCCTGAGCGAGGGGCTGGCTGAAACTGGGCCGGGGCTGCCGAGG
 AGAGTGTGCAGGGAGAGGAGACGGGGTTTGGCCCCGAGGTGCCGGGTG
 GTGCCCTGGAGTGCGGCTGAGCGGGAAGTGGGTGTGGCGTCTGGAGACG
 GGGGCTCGTGGCTTGGGATGGTGACAGACCCCAAGGTGGAGGCGGCC
 GCAGAGGAGGACAGAAAGCCAGGCCCAAGCCCCAGGGCGGGAGGCTGGG
 AGTCAGGAGGACAGAGAGCCCTGGGCTCAGTGTACCGTCTCTGGCA
 CCTCGCGACGGATGTCTGGCCGTGCAAGTGGTGTCCCTCACCTGAG
 CCTGAGAACCATGCAGGATGCTGGTGTACAGCAGGAGAGGGCCAGGGC
 CTGGGGAGGAGTCTTACTGGAAGGCTTCTCCTCCGTTTGCAGCAGGGC
 GGAATGACTGGGG

Contig 92 (694 bp)

TGGAGCCAGGACAGGCAGAGCGTCCGAGGCCGTGCTGTGACCCGG
 GGGATGGGCGACCTGGGGTGGGCTGTGAGCCAGGCATAGGGACCCCG

SUBSTITUTE SHEET (RULE 26)

FIGURE 6. CONTD.

ACTTGGGCACGGCCAGGTGGGGCCGGGCAAGGGGAACAAGGACGCTGGC
CTCCAAGGGCCCCACGTGGGCACAGAGGAAGAGCCGACCCAGGTTGTGGG
CGCATGSAACCCCCACTCTGGGGCCAGGAGGCCAACCTCCCAAGGGC
TGAGGCTGGGAGGGAAGAGTCCCTTTGGGGTCACTCAGTGTCCCTTGTG
GGTGGCCCCCTGCCACTGGCGGCACCTCTGACCCCAACTCCTTGCGGGTG
GACGGTGGATGGATTTCCTGCAGCCTTCTTCTGGAATAGTCTCTGCCAT
CCTCGGGGAAGCAGTGATTGCTCTGCCCAAGTCCAGGCCCGCCCTGCAA
GGTGCTCCACCCCAATGAGCCCCGGACAGTTTCGAGGGCTTCTCACGC
TACTGAGGGGTATGAACAGCTGTCCCCCTCGGAAAGTGGGGGACAGGGCC
CTGCCACTCCATCCTCGGGACCGCGGTCTAGTCAGCACTTGTCTCCCTG
CCTTGTGCCCCCTGACCTTTTTTGGAGCCATCAAAACCTCAGCCCTCG
CCCCAGGAGGTCAAGCCCCCGTCCCCAGCCCCAGACCAGCA

Contig 93 (900 bp)

CCAGCCCCATCCCCGGCTGGTCCCCACACAGAGCCCCCGTTTCCC
AGGGGACAGCAGAGCTGCCCCAGGTCTTACATAAAGTCACCTTCTCAG
AGCTCCTGTGCGGGCTCAGGGGAATGAATCTGACCAAGCATCCATAGGAC
ACAGGTTTGATCCAGGCCCGCTCAGCAGGTTAAGGATCTGGCGTGGC
GTGAGCTGTGTTGGAGGTGCAAGACGTGGCTCAGATCTGGTGTGGCTGT
GACTGAGGTGGCGGCCAGCAGCTGCAGCTCTGATTGGACCCCTAGCCTGG
GAACCTCCATATGCCGCGGGTGCAGCCCTGAAAGGACAAAAATAAATAA
TAAATAAAGAGAGTAAACACACCTTCTCTAGCCATAACCACTGCTCAGG
GGCGAGGGCCAGGAAGCGGCACCCCCCGCCCAAGGCTGCCGTGGCGCC
CGGGCAGGCGGCTCAGCCTGCTTTTTGTCTGTGATGTAGCCGCCCCAGC
CCACATGGAGGGGCTGGGCTGCGCAGTAACTGCTTTAACTGACGGGAGC
TTGACCCAGCAATTCAACAGCGGGCATGAGCCGGGAAGGGAAGTTATTC
GTGTGTAGCTATTAGGCGCGGAGTGAAGGTGTGCTTGGCCCTGGGCCCA
CCCTGGGGGAGGCAACACAGGGGTTTGAACACCTGCCATGAACACG
GGGCAAAAGCCAGCCAAAGGGGGCAGGTGCTGAGGCTGGGAACCAACCG
TGCTCTGAAATCCGGGAATGCCACTGCAGGCATGTTCAAAGGGTCAA
GACCGGGGCTCTGCTTGAGAAGGACTGGCGAAGCCAACTCAAAAGCGC
ACCCCTCTGTGCAAAACCCCAACCAATGGAACAAACTCCAGAGGGGCCA

Contig 94 (550 bp)

AGTCTGGGCTGTGTCCATGGGGTTGCCAAGSTGCCAGGCAGAGACCTTGG
GGACAAAGTCTCTGTAGCAGAAGGACATGGCCACGTCCTCCCTGCTCAGCA
GGTGGCCAGGCTGGGGTCTGATGCCCTCGCTGGGGTGGGGCGGGTTGAG
GGGCCAGGCCAGACACCTTCGTCCTGCCGGAGTGTGTGCTTCTG
TTCTGGAAGGCCCCCTGCAGGTACAGGAGGCCCTGGGGCTGACGCTG
CACCTTCTGACACCTGTGTTCTTGGGGATGGGACAGGACAGGAGACCCC
GGGCTGGACCGGAGCGGGTAAGACAGAGATTGACTCTGTCTCGAGTCT
GTGAGGGCTCTCCCCGGCTTGGGCTTCGTCTGACGGGCTTTTCGGGTCA
GGGTGGCTCAAGGTGACGAAGACCTGGTCTCGGAGTCTGCAGGCGCA
AAAGTTGGAGCCACCCCCCGGGAGGGGGCCCAAGGACAGGAGGGCC
CAGGGAAGTCTGGGGCTGCAAGGCCGTCCGGGCTGGGAAGGCCAAGGT

Contig 95 (1200 bp)

GTTTGCTCTCAGCAGGCAAGGGCTCCGAGGCCCTAATAGCCCATATGA
CAGCGCCGCTCCTGGCATGGGGCCCCGCTGGCATGGGGCAGGGCAGGG
CAGAGCAAGCAGCATGCAGCTTCTACCTTCTTCTGACCTCGTGGCCCT
TCCGAGGCTCAGGGGCTCCCGGAGTGGGACCCAGCCCTGGCTCTCTCT
TCCAGAGCCAGGCCCAAGGCTGGGAGTGGCCAGAGATGAGGTGCCCG
AGCAGGGCACTGCTTGGCGTCCCATCCCTGGCGCTCAGGGCCGTACT
GTCCAAAACCAAAAGAAAGCAGTCAGCAAACTTCTCCAGCAAGCTGGG
GTCAAAGGTGCTTCCGAGGCGTGATCAGGGTGGCCTTTGCTACTGTAC
CGTGTGCCCTGGGAGAGGCACAGGACACAGACACACCTCCGAGAACC
TGGGGCTTCCAGGGCTCAGGCTGCTGGGCCATCCGGGCCCTGTGCT
CCCAGGATCTGCCGGACCGTGAGGCTGCGTCCACCCCTCTGCTGGGA
CAGGCCCCACAGAGCTCAGAGCCAGGGGACCGGGACAGGGCCCCGCTG
GGCCACCTGCTTCCAGCCTCAGCCAGCTGGGGCCAGGCTGTGCTGCTGC
GACACCTGAGTCTCAGGACGGGCGGGGACAAAGCCGCCCGGCCCTCC
CCCGCTGGGAGGAGACCGCGTGGCCCTGACGTGTGGGCTGTGAGAGC
TGAAATGTACAGCAATTAGCCCTAACGAGCCGAGGGAGGGAGCGCGG
GGAGGCGGGGAGGGGATCCACGAGCCGAGGGCCCGGAGCTGGCCACCC
CACCGTTCGATTCCAGGCACTCAGGATAATTGGGTGTTAGAAATCAGG
CGGCAGCAGAGAGCGGGCAGGCGGGCTGTGCCCCCTCCACCGCCCC
TTAACAGGTGCCCGAACACGAGGCTTGGGAGATGCTGAGTCCGCAAG

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SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

AGAAGATGCAGGAAATCCTCAAAGTTCAGTCACAAGAAACCAATTCA
AAAACAGCAGCAGACATACGATGGCAAATAACACAGAGAAAGTCAGC
ACCCGCTGTCCCTGGGGGGACGCGAGTCAAAGCCAGGAGACACAGGAT
ATGCCCACTGCCAAGGCTACGGATAACGGGAAGCAAGACACAGACAGA
AAGGATGCTTCGGTGTGGGGAGGGTGGGGTGGGGCGGGGGTCCCCC
TGGAGCAGGATGTGAAGGCACTTGGGGGGGGCTCTGCACTCCTGGGGGCC
TTTGGCACAGCGGAGGGCCCGGAAGGCTCTAGGGGACGGAGAGGGGT
GCCAGGCTTCCTACCCAGCCAGGAGACAGGCGCTGTATGAAGCT
GACGTGCAGCAGCAAGAGCAACATGCTACAGACATGTGTCTGTGTGTG
TGTG

Contig 99 (1000 bp)

GGTCTCAGCGCCACGGGCGAGGGCTGAGGGTCCGAGGGGCTTGGGTG
CTGGAAAGCCTGAGTTGAATCCAGCTCGGTTCTTAAAGCTGTGTCTC
CAGGGCCAAAGGAATGGGGCTCTCTGGGAAAGGTCTGGGGTGAAGGCTGGC
GGGACCTGCCAGCCCGGAGGGCATCTGACCAGACAGCTTCTCAAGCTCA
CAGGGCTTCATGGCAGGATGGGGAAGGCTGTGGTGGGGAGTGGGGAGCAC
TCGACACCCCTGTCCAGGCCCTTTGAGTCACGGTGGCTCTGAAAAGGGGT
TCTCTGTGTCCATGAGCAAGTCTTTGTCCGGGCGAGGATTACTAAGTCC
AAGGGTGTCTGCCCCCTCCGTGGGGCACAGAGCAGGGGGCCAGATCACGT
GGCTGTAAGTGCAGGTTGCAAGGCTGCCACCATGTCCCACTGGGTCTC
CCAGTTACCTTGGGAGGTGCAGGGTGGGGTGTGGGAAACTGAGGCAGA
GAGCTGCCAAAGAGTGGCGGCAGGGACTGGGGGCCAGACCCAGCTAA
CCGACCCCTCACAGGAGCTGCTTCTACTTGCAGCCTGGAGTGGGAAAA
GGTTACCCACAGCAGCGTGTGACGGCAGCGTGGTATGTCTGTGTACTTA
TGCAATATGTTCTACGTGCATGCACGTGAGTGTGCTGTGTGCAATTGTGCCT
GTGTGTGTGTCATGTGTGTGTGTCATCATGTGTCTATACGTGTGTGTAG
TGAATGCTTGTGTCATGTGTATTTGCATGTGTATCTTTGACGTGTGCACT
GAATGCATGTGTGTGAGTGGCGGCATGTGCGTGTGTGCGCATGTGTCTG
TTTATACCTGTGTGTAGTGAATGCATGTGTCATGTGTGTGTGTATCATGTG
ACGTGAGAATGTGCACTCGTGCATGTTGTCATGTGAGTTTCATGTACACA
TGCTTTTAACTGTGTCAGTGTGTCATGTGTCTGTGTCCCTTGACAGC

Contig 100 (1500 bp)

CGTATAAATATATTAAATAGAATAAAATAGATTGATAATATAGATAAAC
TAAACCCATTATCAATACCGGGTGGCCCCAGCAAAAGGATACTAGCCAGTT
TATCAAGGTGCTAAGTCAGCACATAGAATGGCCACAAACGAAACCTGTA
CTGCCATATGTCCACTTAATGGAGTATGCCACTGACATCAGTGGTAGGTG
AGCTGAGTCCATCTGGGCTCCCAAGTTCGGGCCCGGCTTGCCCCAACGG
AGGTTCCCTTCCAGGGTTCGCCAAACCCAAACCGGGCCCCAGGTCCTCCCTG
TCTTGACTCGTTTCTGGAGTCTTCTGGGGCTCTGCAGTCTCCCTTGTGTG
GGGCTTCTGTCCCCCTGCCCTTGGCCTTGGGGCTCGGCCCTGCCCTGGG
TCCCGGGCTTGGGGCTCACCCCTCCTTCTTCCCTGGAAGAGAGGGAGCC
AGGCTGGGCCGGGCCAGGAGGAATGCGCCTGACTCTGCTCCAGATGGAC
AGGTGGGGACATGCAGTGGCCTCGCCTTGGGCTGCTGAGCCAAGAGCAGG
ACGGGTTCTTTCTGGAATGTGGGGCCAGCCAGGTTACGCGTGTGGGTGGG
CAGCCGCCAGCATCTGTAGGGCCGCTGCAGGCGCGGGGAATGACCTCGA
CTTCTGCTTGGCACCCAGCTCTGGAACAGCCCTTGGCGAGCCTCCGCC
AGAGCTGGGCCAGAGGGTCCCCGTGTGCGGGGACCCAGCAGGGCCCTC
CCTGACTCTCCAACCCACCTGCCTGGGAGGAGTGGCCCCCTGGCCTCCGT
GGATCTCTGGGTCCGGGCTCAGCCGGCTTGACAGCCTGGGAACAGCCAAT
GCACATCCCCAGGCTTGGCCACACCTTCCACCGGAGCGGGCGGATCTG
CATTTCGCCAGGCTCTGCGGGGAGCTCTGAGAGCCCCGGTCTCGGAGCC
CAGCCGTGGCCGTTGTACGCCCTGGGGGCTGTGGACAGCGTGTCTCATT
GCCCTCCGAGGTCCGGCCAGGTCCCTCCACCTGCTCGCCAGAGCC
CTCTCCCCACCAACACACTTCTGCTGTCTGCAAGCGGGACACACACT
CCGGTTTACAGGACCTTTCACAGTGGCGCTTCTCTGCAGAGAAATGCCTG
GAGCAGATGTTGTCCGCACGGCTGCTCCGCGAGGCCCTACCGAGAGCCCC
TCACCTAAACGGCCGGGCTCAGCAGCCCGGGGCTGTCCCCACCGCCC
AGGTGGTGGGTTCTCTGTGCCAGTGTGGGATCTCTGTAAGATACCTGT
TTATCTGCTCATCGTCTGGTCTCCCCAGAGGTAGAGCAGGGCCCGGCA
CAGCCGTCTCGGGTGGCCACTCGCCCTTGGGGCTCAGCTTCCATGCAG
GGAGGACGCGTGTGACACGAGAGCCCGTGTGAGTGTGCGGGCGCCG
AGGCTGCCTTAGGTACAGCCAAAGCCGGCATTAACACACAGGCCCTCGA

SUBSTITUTE SHEET (RULE 26)

FIGURE 6, CONTD.

Contig 101 (600 bp)

TCTAGAAATACCTGGCCCTCCAGGGACGTGCTCTGCTAGCTGCGGCTTTCAG
GGCAAAGTGTAAATTAACATCCCCAGGCTTCCCTTCCAGTTGGCACAGGG
CACCCACATGAGGAGCAGCCTCTGGGTGCCAAAGGGCCCACTGGTGCCAG
GCGCTGGGCTGAGTGCACCCCGCATGCTTCCCGCCACTCACCTGCTGG
CCCCACCCCTGACCACAGCAGCTGTGGGAACACTAGGCTGGCAGCCACA
CGCTGCTCTACTGGAGGCCAGTCCAGGCAGCCTGCTTGGCTACGCTAG
CAGATGCCCGCTCGCCTCTGCCCCGCCCCAGCCATGCAGGAGCCAG
GGTGGGGCACAGGAAGGACGATTGGGGCCCAAGGTCAAGGCACATCCAGGC
CACAGCCGTGGCCACACGAAGCGGCCCTGAGGGGGCGTTGGGGGGCAGA
CCCTGCCCCCGCTGCCGCCAGCTCCAGGCATTAAATCCAGGGACC
TGTTCACCTGGGTGGCGCCAGCCTGCCCTTGCCTTCCAAGGCCTCTA
AAATGCCCTCTTTTCGTAACCTAGGACTTACCAAGCTCAGCGAGCCCTC

Contig 102 (1867 bp)

AGTATATCGGGTGAGACTGGGACCGGTCTGCCGGGAAGCCCCACCATAA
AGGCCACGTTGGGCCACAGTCCGGGCCACGTGAGTGTGGGCGGGTCCGCG
GGTCTGCTTGGAAACACAGGATCTTAAGAGGTACCAGCCGAGGCCAA
GTTACGCTGAGCAAGTGAAGAACTGACTGAATGAGAGCGTGAGCGAATGA
GTGAGGGGTGAGTCCGTCCACACGACGCTAGGCTCAGCCAACCGCTGT
CCCCCGCTCTCCACTGGTGACCAGAACGGAAAGAGTGGGAAAGAGTGGT
TGCTCTCCCAACCCAGTCCCAACCCCTGGAGCCCAACCCCTCCAG
GGGTGCCGGGCTGGCCTGTGGGCCCAAGTCTGGAGGCTCTGGCACCTTC
CTCATCCGTTCTCCAGCACCCAGGTTCTGTCTGAGCCCTCTGGCCCA
CAGGCTCGGGGACAAAGAGGGCCACCTGGAGGCTCAGGGAGCCTCACCT
GCTCTGCTGCTCTGCCGGAGCGGGTCTGGACATGTATAGACCGGCTG
GGCTCAGCAGCTCTGCTGGAAGATGTACAGGACAGCCTGGGCCACTCTC
CCACCAGGAGAATTATTCTCGTGGGTCCCCCGGGGAAGGGATGGG
ATCCAGCGGGGACCCAGAGCGTCCAGCACAGGACCTGTCTCTCCAGC
CCCTGCCCCACAGGATGCTCAGAGCTCAGCTCGAACACGACCTGTG
GACTTTGCCCTCTGAGGCTGTCTTCTCAGCCGACGCGGGCTCCGCTGCA
TGGTCTGGAAGCCAGTGGGACTCGGTGTGACAGGGAACAGGGGCTCTT
GGAGTGGGTGGCGGGGAGCCCGAGGAGCTGCTTGGGCTTTGATGG
CTGAGTGGGTGAAGTCAAGGAGGCTCCCCAGGGCTCTCTGACCCCCC
CACCTCAAAAAATCCAGAGCATCTTTGCTTGGGTCTGGTGAAGCTCTC
TGAGGTGAGACCTGCGTGGCTGGGCCAGTGGGGCTGGAGCAGGAAGAAA
GCAGGACAGCCCCCGCCCTGGCCAGACTCCCCAAACCCAGCAGGAGAC
ACCTGAAACGGGATGGAACATCTGAAAAGAGCCACCTCTCTCTCTTA
TGATCAGCTGCCGGGTCTGGGGCCCGCCAGGCCCCAGATGTCCGG
GCTGCTCCCGTCTCAGATCCAGGGTTTCTGGGCCAGGACTCTGTCCCC
CAAAGCATGCAGAGGTTCCAGGCTGGGTCTTATGCTCTGCCGTGTGCA
TGCTGGGAAGGAAGGGGACAGTCTGGAGACCCCCGCTCTCCATGCG
TGGCGCCGGGGACAAAGCCGCTGGGGTCTCAGGTTTGGGTTCAAGCA
AACGTTGATCTGACCTGGTCTGAGATGCTCGGCCGATGCTGCGTTGTC
CGCTCGCATTTCTCTGTTTCTCTGGGAGGCGCTGCGTGCCTCTGGCTT
CCGGCCAGCCCCACGAGGACGACGGGTGGCTGGCGGGTCTGGGGGCC
CCTGCCCGCACAGAACGTCTGGCTCAGGTTTGTCTCTGACCCATC
ACTAAGGGCCACCCTCTGACCCGAGCCCTGTCTCCGAGGTGGGAATTGG
GGGCTGTCTGGGCTCATAGGACCTGGTGGGGGCATCCAGGGCTGTGT
CATGCCCTCCCCAGAAGACTCTGGGGGCTGGGGAGGGTTTCCCCAGCT
TCGGGGCAGCTGGGGGCGGAAGGCGCTGGAGGCTTGCCTGTCCCA
GGAGCATGGCTTCGCTGCAGACTGGGGCCCGCACCCAGCCACCACT
GGCGCTCTGGAAGCACT

Contig 103 (650 bp)

GTTGAGGATTCTCGGCAATTCTCTGCTACTGGCGCTCCAATCGCCTCG
ATGGGCTTCTCTCCAGATACAGCTGCAGATCTGGCGGGCACACCGTT
GAGCGTCACCTCGTAGTGAGATTGCACTCGTTGTCAATGGACATCCAGG
CCATGCCGACGGCATGTGGATTCTGTGCATCCGTGTGCTCTCTGCTTC
AGCAGAAATGGGTTCGCCGAGTCCCGAGCATCGGCCACTGGAGCGGGCAC
TAGCGGGCCACGGATCAGGCTCGTCTCATGCTCGGTGGCCACATTAACGC
CCAGTTCCGCCGATACAGCGACTCGAGGACCTTGGGACCCAACTTCTCC
ACACTACCAATGGCTGGTTGAAGTTGAAGCTCGGCGTCAGATCTCCAG
CTTGGCCTTCCGCTTGCCTGTCTCAATCAAACTGATGTTGGGCCTAT
CCGGGGTGTTCAGTGCTCCGTTTCGATGTTGAGGCCAGAGATCCATCG
GTGTTCAAGTAGACCCACGCCAAACCCGCTGCTTGGTCGAGGATTCCGGC

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FIGURE 6, CONTD.

ACTGTGCGGCGCCAGCAGGGTCTGGAAGATTTCGACGTGGCTCGGGTCA
CGATGTGTCCTGGATGCGCAGATGTGGGTACTTCTGGACTCCACGGTC
Contig 104 (1630 bp)
GGTGTGTCTACTGCTGTGGCTCAGACCCCTGCTGTGGCACAGGGTCCATC
CTTAGCCAGAACTTGCACATGCCACAGGTGCAGCCAAAAGAAAATTCT
TACTAATAAGTTGTTCAATTGCTTTACGTAGAGTGGCATCAACAGCAA
ATTTAAAAACCATCTATCAATACATAGACCGGGTCAAAGGGAAGAAC
TTTCTATTTCAGCACCTTAAACATGGCTTTGCCGAATTGGGACCAGGG
TGCTGTGTTTTATCTCTCCCTGCAGGTGGTCCCGAGATGACCAGGCCG
TCCTGGGCGGAGGAGCCGACTGTGGATCCAGTTGCTTCCCAAGACAGG
CTGACAGGAGAGCAGCAAGGGCCACCCCAACCGAAACCAAGCCAGAAC
GAGCAGAAAGATGCCGTCTTCCAAGTGGGGGTGGGAGCTTCTCCCATC
CTCCGGAGCCGTGAGGCTGCCCTGGAGCTGGCAGGAGCCACAGAGGACCC
GGCTTTGACCGCCCTCTGGGACCCACAATCAGGACCTGACTCAGATGC
TGAGGGGCTGGACAACACCCAGGACCTGCTGCTTCCCAAGAACCGCT
GTGTCCATCAAGTCCAGATGGCACCCTGTGCCCACTGGAGACGCACT
CCGTGGGGCAGGCTTTCCCTTGGGCACCGATGCACCTTGAGGCGAGAGAC
GGGGCCCAATAAACGTTTCCAACACAGTGGGTGAGGACCCGACCGGCC
GACACGGCAGCCCGGATGCAGGACTCCGTGCTTGGCCAGCCTCCCTTG
GGGTGGTCTGTCTCTCAGGGTGGATAGGCCATCATGTGGTGGCTC
TGGGGACATCCGTCTCTGATTGGGTGAGTTTCAGCCACAGAGATATTCC
CAGGACTACAAAGCTGGGTCCCTTGGGGACCTGCTGTCAAAAAGACA
AGGCCCTGACCCCAAGTAGCAAGTTCCCCAGGGGCTCCCAAGGCTCG
GCATCCAGACTGTGCCAGCGTGTGCCCGCCCAAGTCTGCTGACCC
GAGTCTCTGTAACATCCCGGGCCCAACCCAGCTTTACCCCAAGGCCGA
AAGCACCAGCCCCCTGCACCACAGATGAGGCCCCATGGTCCCCGACC
TAACCTCTGTCTGCAGTTGGCTTTCAGCCTCGGGTGGGGCAAGGCCTGC
ATCTCAGGCTCCCGGAGAAAGTTGCTGCCCTCCACAGCAGAGCCAGGGCC
TGTCAGCACCTGGGCGGGTCCGATCTGCTCTAGAATGCTGCTAAGGTG
TCCTTGACAGCAGCCCGGGCGGCCCGCCCTCCAGGAAGGAAGGGGACA
TTGCCAGGACTCAGGAATGAAGCATCCAGGTTTTGAATCCCGGTCCTC
ACCACCTTCCACCTCTGACCTCAGGCACCTCGGCTTTCAGAGCTGCCCTT
TCTGACTCTGGGACACGGGCTGTGAGGCGCTCTCGGTGTGTACAGCTG
GGGGGGGCACTCTCTAACGAGGGTGGGCGTCCCAAGGTGACTGACCACA
GCCCTTCTCTCTCAAAAACGCCCGCCGAGTGACCTCACGGGAGGCAG
GGCCAGGAACCCCAACCAACCAAGATCA
Contig 105 (1820 bp)
AGTGAGCCCTGCAGGACAGTCTGCTGAGGGGTGTCTGGGCTCCTCAGAGG
TCTATGGCCACGGGCACTGGGAGGATAGCAGGTGGACCCCTGCATCCAGG
TCCAGGTCCAGGTCAGAGCCCGGACAGGCTTTCTATCTGCAGGAG
GGGGCTCCTGGGGCAGCAGGGATGTGGCTGTGAGGCTCGTCACTCTCC
CTGTTTCTATCTCTCTCTGTATCACACACACACACACACACACACACA
CACACACACAGCAGCAGCAGCAGCAGAGGGCTGACAGGGCTGCA
GACAGGGCATGGGAGGACTGCCCGGAGTGCACCCAGATGGCCACAGG
TGGGGCCCTCGTCCCACTTTTGTCTGATGCTTCCGCCAGGCTGCTGG
GAGCAAGCACTAGCTTCCAGGGCTCTGACCAGAGAGGATGGGAGGGGT
CATGGGTCAACAGGCCGCCAGGGAATGGGGAATAGGATCTGAGGGGCGGG
GCAAGGGGCCAGGCGAGGCTGCAGTGCCAGAGCTCCCTGCACCTGCAG
GACCAGCCACAGGCCAACAGCTGCAGGCAGAGCAGGGCTGCTCTGTCCC
CAGAAGCTGGCAGCAGCATGGGGTCTGACAGCCCCACCCGGGCTCCC
ACAGAGGGGCGGGTCCCCAACTCTCCCCCGTCCCACTCACAGCTCA
GCATCTCCACTGCTTGAGGACGAGCCCAACACAGGGCACACACACAT
GCACGCACACATGAATGCACCTGCAAGCACACACTCACAGTAAGCAG
GTACACACATGCATGCACACAATGAACACACATGCACGCACACACGATG
CACACAGCAGCAGCACTCAACACGATACATGCAGCAGATGCTGGTCTT
TTGTCCCCGTGGAGGGGAGGATGGAGGCCAGCCCGTGGGGAGGGCATGT
GGAGTGTGGGGGCTGGCTCCAACGCCCTCGCTCAACAGGCACCAACGC
TGGACTGAGATAAGCGGGGGCTGGCTCCCTTGGGGCGCTCAGCAGGT
TTGACGCCACCAAGGTGGCACTGCCCTTTTCAAGACGGATGTGGCC
ATGCCACCTCAGCAGCTCAGCAGTCCCCCTCAGCTTTAGTGGTGTCCC
TGTCAGTGTACCGGGGCTTCTTCTTCCAGGGCCAAAAGCGAGTTTCA
GGGACAGTGGCGCCCATTAATTACTACCCAGGGTGTCTCTCTGTGG
TGGCCTTGAGGCCAAGGTGCTCCATGGGGGCCACAGGGCTGGCAGGGT
CACTTCTGAGAGCACCCAGGGCAGGGGGTGGCCAGGCTGGCCCGT

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FIGURE 6, CONTD.

CCCCATCTGGAATGAGGGCCTTGCGCAGAGGCGGTGCACCCCTCTTTACA
GCAGCCCCGGGGGAGAGTGACTCCTGCGTCATGGACCTGGGGGCTGACCT
GTCACGTGTCTCGCCAGTTGCACCCATCCATTTCCGGGTGGAAGGGAC
AAAGCCATCCTGGTCTCTCAGAGGACCTCGAGGCTCTTGGCCCCAGC
AGCCAGCCCCCTCCCGGGCCGCATCCTCTGCCACCCAAAATCACCTGT
GCCACAGGGTCCCTTCTGGGTGTCCAGGGCGACCCAGAACTGCCCTG
CAGACACACCCAGCCAGGACATGGCCGCTTGCCGGGCTGTCTGCCTG
GGGCAGCCTGACTGCCACAGACAGGCCGCTTGAGGACCATCTGCCTGAG
CCCCAAGGCACATCCACGGGGCCACACAGCCAGCGCTGTAGACGAT
GCCACTTGGGGTGGGGGAG
Contig 106 (1500 bp)
TGCCGAATAGAGGTGGAACCAAGACCCGAAAAATGTCCACATTTTCA
ATTATTAGAAATTTAGAAAAATATTTTACAGGAGTTAAAGGTATTCAT
TCTGGGGGGGGTGGGCATGCCACGGCATGCAGGCAATCCCCGACCCAGC
GACTGAACTCGAGCCACGGCAGTCACCATGCTGGATCCTTAACCTGCTGA
GCCCTTGGGCAACTCCAGACACTCCATATTATGTAACATATTTTAAAC
CAAAAAATGACAAAGCTTTTCAAAACAAACACATTTATGGGAAGAGT
GGCATTGCTTACGCCCTGGATGGTGGCTGCGGCTTGCGGGACGACGAGGG
CCCCCGGGGAGCGCTCCGCACGGCGCATCAGGACGTTGGTCCAGGGGA
AGCGGGGTCACTTACGGGCTCTCGGGTGGCGTGGGTTCCTTTTCGGC
ACCACACCCGGACTCAGCACTTGGGGGTCTTAAACGTGAGAGGCACTGC
GGGGCTCGAAGCCACATCACTGACCTCTCAGACTCTGTTATGTGAAAC
CCATCCGTCACGAGACCAAGAGACAGACGAACAAACGCAAGGTGGCGC
CTAGGTTGGGCACAGCATGAGGGCAGAGCGGAACCTTGGCGAAATCCCG
GCCAAGCCTGGACGTGCGCAGCTCTTACTTGACGAAACATAGGGGGATT
CAGGAACTCTTTTACCGCATTTGCAATTAATTTGCTGCAAACTCAAAAT
CGTTCAAGCACAATGCTCACTGCAATGGAACCAACCGGGGTAGGTCTCG
CCCGATCAGGATGTTTCCCGTGCCCTCTGTGCGGGTGTGCCCCCTGGC
CTGGTCAGTGAGAGTGTCCCTCCACGACGACATGAAACTTCCAGGTC
CAGGCTCTCTGCTGCTTGGACGAAACTCATCTCTGTAATCTCCCGC
AGTCCCGGGGAGCCTTCCAGGGCTGGAAGGACGGCGTCCCGTCCAGG
GGCGAGGTGCAGCTTCCCAAAGCTCCGCTCTGCTAGGACGCTCAGAC
GGCATCACCCACAAACCCACGAACCTTTCCCTCGAGGGCAGAGGCTCG
CCCTTCTCCGAGAAAGCAGCCCGCACAGCTCAGCAAGGGGCCAGCTGCGT
TTGTAACCTCAAATGGCCACATAGAGTTTGTCTGGAGGCACGGGGTCTGT
CTGGGCGCCACCACTGCACACGCAGAATAGTGGGACAGCTCCGGGGT
CCAGCTTCTGGAATTAATAAAGTTTACTGCTTCAACAGTACATTCTTA
AGTGTAGCTGGCCCGCAGCCTGGGCGTCCGCTCCGAGGCTGCTCTCTGC
CTGGAACCTTGTGCTGGGGGACCTCTCTCCAGCCCAACCCAGCCCCG
AGCCAGGCAACATCTTCTTGAAGACACCCGCTACCTGCCCCCTCCCG
TTCTCTTCTCTGGATCCAATCTCTCCGCTTCTAAGCTCTCTTGAAGGT
Contig 107 (550 bp)
ATGGCACTCGCGGTGTGACTGAGCTACCGGACGGCGGAGCAGGGCCAC
GAGGGCGACAAGCGCGGGGCTGAGAACCTGTGCGAGGGCAGGTCCCTGCG
GCTGCAGACAAGCCTCTATCGCAGGCCACAGACAGGAGCCCCCGTGTGA
CCCTCAGGCTGCAGACCAAGTCAAGGCTCTGCTGGGAAACCTCGAAC
CTGATGACTGGGTGGGTGACCCAGGACCTGAATTCCGGCCTCTGCAGA
ACGCTCTGAGCCTACGGGAGTGGCCACCTCTCGGTAGGGCTGTGTCC
TTCCCTGGCTTCCAGCCTAGAGCAAAAGCATTAAATCAGAGTGTGGCCCA
GCCCGGACCGTGCAGGACCTTAGACAAAAGAGGAGGGAGAGAGATGAG
GCAGAGAGGAGAGAGACAGAGGTGGAGAGACAGATAGACAGAGACAGAG
GCAGAGAGAGAGACAGACAGACAGAGACAGAGGGCGGAGAGACAGACAG
ACAGAGGTGGAGAGACAGGCAGACAGACAGAGAGGCGGAGAGAGACAG
Contig 108 (900 bp)
TTTCTAACTCTCTTACTAGTTCTAGTTTCTATTGTTTTCTGGGGGGT
TCTATATAAACATTCTGTCTGTGATTGGAGATGGTTTTGTTTTCTCT
CCAACTGTATGCCATGTGTTCTTTTCTTGTCTTATCAGACTGGCTAG
GACTTCCAGTAAACACTAGATATGAACATGAGAGGAGAGCCAGGCTT
CTTCTCAGTCTTGGAGGAAACAGTCAGTCTTCTCATTAGAAATGAGAG
CTTTCTTTTCTTTCTTTCTTTCTTTCTTTTCTTTTCTTTTAAAGGT
AAGGAACTTCTCTGTATTCTTATTTTTAGAGTTGTTATTTTTTTT
CTCTTTTTTAGGGCTGCACCCGAGGCATATGGAGGTCTAAGGCTGGGG
TCGAATTGGAGCTACAGTCGATGGCTACGCCACAGCAATGTGAGATCTG
AGCCACATCTGCGACCTATACCACAGCTCACAGCAATGTCAGATGGTTAA

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CCCATCGAACACGGCCAGGAGATTGAGCCCGCATCTCTCATGGATGCCAGTC
AGTTCTGTCGACCGCTGACCCATTGACGGGAACCTTCCAAATGAAGCCAAATT
TTAAATGAAAAGACAAAGCATTCAGCCAGCCAGCGCTGAGTAAGGAGTTTG
GAGGCGCTGACCCCTGCGTGGTCTGCGGCTGGGGCTGGGCTGGTCCGGGGT
GGGGGGGGGGTGGGGGGGACCTCTGGGACCTCTCCTCTCAGCCAGGCGGCTG
CCCCCTCAACCTCTAGCTTCTGGGGGGCTCGAGGAAGGCGGGGTGGATGACG
GTCCCTGGGACCCCTCTCATATGTATCTCGGGTCCCTGGTCTCTGAGG
CCAGGTCAGGTCATGGGATCAAAGGTCAGCCAGGGGGTATGCCACGAG
Contig 109 (950 bp).

TAACCCACTGACCGAGGCCAGGGATCAAACCTGCAACCTCATGCTTCTCTA
GTCGGTTCGGTAACACCTGCGCCACAGCGGGAACATCTTGGCTTTGTTT
TAGAGTTTACATACACGTGATAACGTGCGGTATTTATCTTCTCATCT
GAATTATGTTCACTTAGCTCAAGCCCTCAGGGTCATCATGGTGTCTGGG
AGTTGACGAGTTAGCTCTTTTTTTTTTTTTTTTTTTTGTGGCTGAATACG
TCCAGGATTATCTTCTTTTTCTGTTTATCTGTGGAGGACACAGGCTGGCT
CCGTGTGACGCTCTGCGGGGAATACGGGGCCGATCGCTTTCTAGGCCAC
TGTTCTCAATTTCTTGCGGAAGTAGCCCGGAGTGGAACGGCTGGGTCTGT
CTCGAGTTCTGTGCTGCATTTTGAAGACAGCTCGGAGCGCTTTCCACAG
TGGCTGCACCGACTCAATCCCAACGAGTGCACGATTTCCCACTCT
TTTTCCACGTTTTCCCGCACTTGCTATTTTTGCCCTGTGGATGTGCGCC
TCTCCGTCAAGTGTGAGGGAGTCTCCGTGCGGCCAGCGGAGGAGGACG
CGTAGCGCTGCTTTCACGATCTCTGTGCGGCACGTCGGTGCTTCTCCGG
AAAAAGGCTGTGTCAGGCTCTTCCGCCATTTCTCAGTCTGATTGTTGGG
GGGTTTGCCTGTGAGTTGTGTGAGTTCCCGACAGTATGGGGGCACTCAAC
CTTTATCAGCTATGCGATTGGCAAGTCCGTTCTCCCATGTTCCGCGCGCC
GCTTGGACAGTGTGGGCGGCTCTCTTGGCTCTTCTTGGTGCGAGAAGG
TCCGCTCTGATGTGGGCGCAATTTGTTATCTTCTTTCTTCTTCTCAGCT
TGTTTGTGATGTCAGATGCAAAAATCCATTGCCAGGGTCTGTGCCGAGAAC
Contig_110 (306 bp)

Contig 110 (306 bp)

CGCCACCTCTAATCGCCGGTTTGTTCTGCAACACGGTCCAGATAAACCAGCG
CAGCTTACAGGTCGGAACTCGCCAGAACTCGGAACACGGCGGTTTGAACCG
ATCGTGTTCAGCGGATCGACCGCAACAGCGCAAAACAGCGCTACTTGCCAG
CAATCGGGACATCCCGGTTTAAACGTTTGGCGTTTGCCACTGCTTACGAC
CCAAACATCTCGGAAGAGCGCATTAATCAGCGCGCGACAGTCGTCGGTGG
GCAAAACACCCAGCAGCGCAGCATTAATTGCGACATACGGGTTGGTGAA
CAGGCC

Contig 111 (800 bp)
GTTTTCATGATGCCACGAGGGGGCGGGACCGAGCAGGGAAGGCTCCA
TCTCGGCTCTGTAAAGACCTTTGAAACACCTCATTCCTCTGGTCTTGGCCCT
GCTCTTCGGTAGCCCAAGTTGCTGAGACTGATGTGGGATCAGTGGGGAG
CAGGAATCTTCTGATCTCAGCCGTTTCAAAGTGTCCCAAGCAAGCTGTG
GATGGCAATGCCAAGGCTATCCATGGAGGTGGCTGTGCCAGGGGCCCCAT
TTCTCGGGAGCCCATCCAGGAAGAAGTAATCTTGATGCCCCAGGCTCCAGC
AGCCAGTGCACGGCCCTGGGACTATCCGGGTAGATCAGAGGGAGGAACA
GAGCTTGTTGATGTGAAGCAGAGGTGGCCCAAGTCCAATTATGTCTGTGCTC
CCAGCAGGGTGGCCAGGAGGCCCTCGTAACCTTAAAGATCTTGGTCTG
GTCAGCTAAATTGTATGACCATTGTACTGAGCACAATCCCGTTTAAAGTA
GAATTTTCAAGGATGACTAGGATTTGCCACCTGAAGCGAGGAAGGCGCT
TCAGGCAAGAGGTACAGAGTGTAGAGGGAGGCGCTGTACACTTTTGGCCGT
CAGAGGGGGTTTATGTGTGACTGTCAGCTGGCACAGTGTATGCCAGGCCCT
GGCACGGCTGTGTGGTGTGTGGAGAGGAGGAGGAGGTGAGTTGAGCCCT
AAGGTCTTCCAGGCCAAAAGACTTGAGGTTGACCGCGCTGTTCGGGGCTG
GCCCGCAGACAGGAGGGAGCAGGTGGGAGCTGCGCTCTGTTTCCGGGGAC
Contig 112 (3062 bp)

CACACCCCAGGAGAGGAAAGACCCACACAGTCCTGATGACAGCTTGGCTC
GGGGCTGGAGCCGCCAGTTATAATGTCCATCAGCAGCTGTGTTCTGTGA
GAGCCATCAGTGGGAGGCCAGGCCAGCTCAGCAGCCAAAAATGAAGAG
CATGGTCTGGGATTTGGCCCAAGCAGGAGGCCACAGGAAGCCACATAAAC
AAGGACCCACCCCTCTGTCACTCCACCAATGTCAATTCAGGTCACAC
CCTGGTCTCGGGGAGGTTCCCTTAAGATCCGGTGGCAGGGGAGGAAAA
GTCTGACTGTGATTCCTTGACAGGTGTATCAGCGGAAGGCCAGGAGGATG
CTCGGGCATGCCACCTCCAGGGGCGATGGTGTATGCACAGCATGGCA
GTATGGGAGAGGACCTCCCGCTGGTGCAGAGCTCTGGGTGCTGTAACTGG
CTTATGCAATTCAGATGCCAAGGAAAAAACAACAACATCCACCCCGAC

FIGURE 6, CONTD.

AGCTTTAGGCTGTTGGTCTAAAGGTCTGCTCCTGGAAGAGACACGCCT
CTGTCAGCGGACACTGCTAAACCTAAAGGAAGAACTGCCACCTGGTCACG
GGACTTCCTAGGCCAACCAACCTACAGGTGACGGCCCGGAGCATCACGAG
GAGGTAGGGGACGGGAAGGGATGCATTTGCTGCTCAGCGGATCCACTGGG
GCGTTTCTGGAGCCCCACGCCACACTTTACTGCAATGCACAAGCCCC
AGGCAGCAGGACAAGTCACAGTAGCTCTGGGTTATCCAAGGAGTCAGGGA
CCTACCTGGAAGAGTCTAGAACAGGTGACAGAGGAGGAGAGGATGGTAC
CAGCAGTATAGGGAGAATCAGAAATCTGACCACCCCTGGGGGCTGACTG
ACTCCCAGACCAATGCCACACTCAGGTTCCCGCTCTGCTGCACTTCCA
GGGTGGGCCACGGGAGTTATGGGCCCAAGGTAGCATCAGAGGCTCCAG
GTACAGGCACAAGCAGCAACCAAGGAGGATCCAGGCCAGGGAGCATCC
AAGAAGCAGCAGAAGCTCCACCTTAGGTACAGTTCTGGCACCTCCAAGTT
GAGAACATGTCTTAGACAGTGCTGACCCCAACCAATGGAGTGTCTGGG
ACTAGACTAGGCACGCCATTTTGGTCCCAGGTTGCCCATCTGTACAAAG
GGTGTGGGCCCCAGGGGGACACAATGAGTCCCATGGGAAGGCTCTTG
CGAATCTCCTTAGAAGCAGATGTAGAGGTGACGTCCAGCTTGTGCTGG
GATAGAAAGTGGAAAAGCACCCTCCCGCAAGGATGAAGCAAGA
GGCACAACAACCTGAAATTTCCCAACGCCCTGGAGATCCTTGGAGAAC
TGGGATTTCCACCTGAGGGGCACCTGTGAGGAGAGGCTGTGTGAGCAC
CTGTGACCTGGCACAGAGGATGCCAATACTAAGAAGCATCAGCTAAAA
GTCTCCAGGAATTCCTGGAAGCTGAGGAAGGGCTCAGGAGAGGGTACAGA
AGCCCTGGGGCTATAGATATAAGGGACGTGCACACCCACTTCAGGTCCC
CATGGACCCAGGGACATTCACAGTGATGGGCAAGATTTCCCAAAATGCAC
CCCTTGTGTGGGGCTGGTTCCGGTGGGTGACGAGACCCACACCAAGG
CACAAAGCACACACCTCAGGCTACTCTCCTCCCTCTCCTTGTGGAA
TGAGCCTTGAGATGCTGGGGCACGTGAAAACACTGTACACTTAGGTCC
TGGTGAACACTGACTGGGCCAGCGGAAAGAAATCATAAAGACCTACACC
CACACACAGCCTTAATTACAGCTGTGACTGGGGCTGGAGCCCCAAGATG
TCTACACCCATAAGACATAGCGTTAATCAGAAAACCAAGAACAGCCCCAA
CCCCACCCAGGCTGACAACTAACAGGTATGTTGGAATATCACTGGGA
ATGTTCTAGGAGTGTAGAAAGACACCAACTAGGGCATGTGCAAAAGAT
AATACTTACGCTGGGAGTGGATGTGACACAGGGAAGCAATAAGTGAT
GGCAGAGGACTTTGATGTGATGATGGAAGCCACAAAACCTTCTAGCTTA
GCTCCATTCCCAACAAGATTGACTGCAACCCCATGCTAAAACACAGCA
AAAAGAAAGAAATCCTCATTTCCAGGCATAAAATTTTCCCCAGTCTCTG
CTGTCTCCATAAGATGTCTGATTTCAACAGGAATTACGAGGCTATAAGA
AAGGCAAGAAAAAACTACACACTGTCAAGAGAAAGCCATCAGAAATAACCA
GACTCGTAGCACAGACACTGGAATGTGAGGATATTTAAATAACCGTGA
CAAATACATTAAAGATTCTAATGAGAAGGGGGTAGACATGTAGATCACA
TAGATTTAGCAAGAGAGATGAACTCGAAGGAAATTAATGGGAGCCCT
AGAGTGAAAAACACTGTAGCAGAGAAGATGGGTTCATCCGTAAACATGAC
ACAGCTTAGGAAAGAAATCAGTGAACCTTGAAGACAGGGCCACAGAAATAT
CCAAACTGAAATGCAAGGAGGAAATAATGAAAGGGGGAGAGAGAAAA
ATAAAAGAACAAAGCATCCAAGAGCTGGAGGGTGACACTGAAGAAGAGAG
CATAGGCATAGCTGGAATCTCAGAAAGAGAGAAAGAAATAACCAAGATG
TAATGGATGAGAATTTACAGAAAGCGTTGTCAAGCAACAAACCATACATC
CAAGAAGCTCAGAGAACACCAAGCAAGGTAACTGTAAAAAAATAGCC
CGAGGTATACCTCATTCAGGCTGTGAAAATCCATGACAAAAGAGTCTT
GAAAGTAGCCAGAAACAGAAGGCGTGTTCATTAGAGGGGAAAGACACC
ATTGTTGCCAGAAACCAATAAACACAGGCTGAAAGGGTAAACCTTTTT
TTTTTTTTTTTTTTTTTGGCCATGCCTGTGGCATGTGAGGTTTCCCGA
TCAGGGATCAAC
Contig 113 (1300 bp)
AAACGGATAAATACAGGTGACCCACAGGCAGAGCTGAAGTACAAACAGT
TCACAACGGCACCCAAAAAATACCGAAGGCTCAAGGGTAAATCTGACCCC
AGATGAAAGGCCTTCTCACGGAAATGGCAAGTGGCGCTGAGAGGCATG
AGAGGTTCGAATAGATGGAGGGCTCCGCCGTTTTCCCGGCTCCGAGGATT
CAGTGACGTACAGAGCCCAATTCCTCTGAAACGCCCTCTAGGTTTCACTG
CAGCCCAGACCCACTGGCAGCCGCCCTCGCTGCAGAGACAGCCAGCTGG
GTCTTGAGGTTCTACAGCGAAGCAAGGCTCTAGAAAAGCAGAGCTCT
CTGGAAAGGGAGAGCAGCCGATGGATTGGCATACGGCGCAGGAGATTCT
CTCGACAGTGGCACCCAGGAGAGGGGTGGACAGAGACTGGTGCAACCGAG
CGGGCCAGGAATAAGTCCACACCCACACGTACCATCTCGTTGTTATTT
ATTTTTTCTTTTTCAGGGCCACTCTGGGGCATGTGAGGCTCCCCAGCC

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FIGURE 6, CONTD.

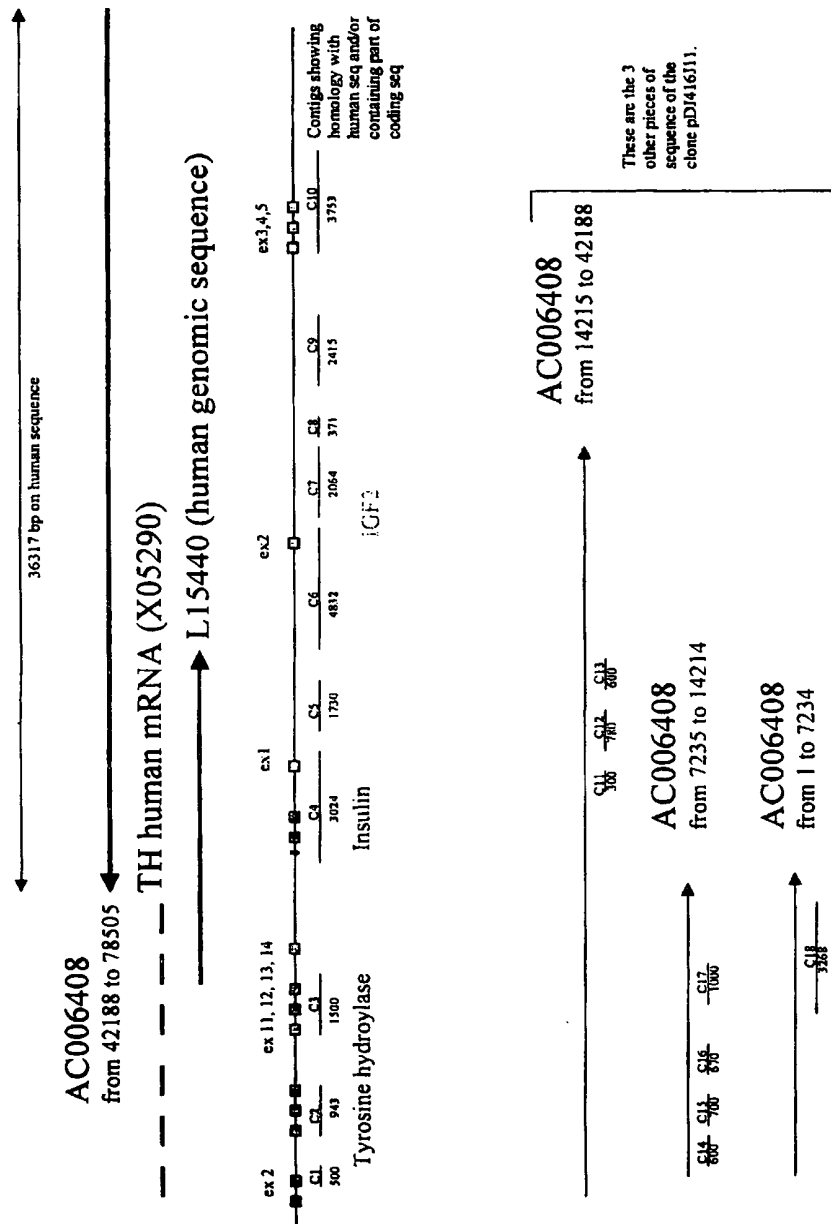
AGGAGTCGAATCGGAGCTGCAGCTACAAGCCTACCCACAGCCACAGCGA
CACAGGATCTGAGCCATGTCTGCAGCCTACACCACAGCTCCCGGCAATAT
TGGATCCTTAACCCACTGAGCAAGGCCAGGACTGAACCCACGTGCTCAT
GGATACTAGTTGGGTTTGTACCAGTGCAGTGGGAACTCCTTTAA
TTTTAATTTTGAAGGTTGAGAACTCTTAATTTTGTAGTGAGGTATAGA
TTATATTACGCACCATTTCTTTCTGACTTCGGTGCACGGCTTTTCAACAA
ATGGGTGCTGGACCTGCTGGGTGCCTTCTCAAATGAACCAACAGCCCTC
CCTCGCGCGTATGCAAAATTTAACTCGAGGGGCTCATAGACATAAACGT
AAACTCTAAAGCTATAAAATTTCCAGAGAAAACGTAAGGAAAACCTTTG
GGGTCTTGGGCAAGATTCTTACCCATGACAGCAAAATTACAATCTACA
GAGAACTGGTGGCCTTTATCGGCATTAAACACCTGCGCTTTGAATGA
TGCTGTGCAAAACCGAACATGCAGCAAAACGATGCAACTAGCAGGTCT
CACACTCACTGACCCACGTGAGAAAGGAAAGACACGCCACGTGACATCC
CTTAGATGCAGATGTAAACACGGCCCCGTGAACCGACCTCAAGAGAG
AGACAGACCTACAGACGCAGCAAAATTTGGGGTTGCCGAGGGGATGCCGG
Contig 114 (3000 bp)
TGTGAGACCCCTTGGCGGGCCAGGACCCCAAGTGACCGAAGGCTCA
GGGCCCCAGCGCCCATCCCTCTTTCCGACACAGGATTTTTC
CACCAAGCTCTGTTCCCTTGGTCACTCTCACTTGAGCAGCTCAGGGT
CTCCCGGTGCCTGTATCCACGACAGCGTACCTTCTTGGTGTCAACCC
AGGACCCACGCTGGCCAGCCACGCTTCCAGAGCACCCCGCCATCC
TCAGAGTCCAGAGGAAAGGCCCATTTGACCCAGAAACCAACGAGCA
GACTCTGGGACGCCAGCAAGAACGTACTGACTCCACCTGCTTCAGGC
ACGGAGGCGAGGGTGGGTTATGAGCGACCCGTGGAAGGGCTCTTGTG
CATCGAGGGGCTTCCAGGGGCTCTAGACGGGATGAGTGTGGCAACATG
TCGCGCATTTACAAAAGACCTGCAGTGTCTGGGATGGGTCCCGCGG
TAGAAAAGCAAGGATTCCAGCCCACTGAGTAGGAGCGGCTCGGAGG
CTGCAGAGGCGCGGGGGGCTGACCACTCGGCAAGCCCGTGTGG
AGGGGACGCCCGGCGGGCTGCAGCCGCTGCGCTCCGATAGCTCTTA
AGAGCGCGCTGCCCATGACGCGCGTGCACACTCGCTGCCCGAGGG
TCCTTCAGCAGACCTTGTGGGACGAGGACCTGGCAGGGGTGTGGCT
TGGGGAAGGGGTCTGTCCAGGAACCTGTCTGGATTGGGGGTGGG
GTGGATATCCCGTCCCAACCTACAGAGGAGGGGCTTAAAAGAGCCCC
TTTGGTGTGAGGGGCCAGCAATCCTTTGGCTTTTCTTGGCCACTTGG
GCTTGACGTCTGGTCACTGACTGGGAGCCAGGGCCAGAGGGGGGAGCG
GGCTGAGGAGGTTACGGCCCAACATCTCTCGGCCACCTCCGAGGTCG
GGCAGCTACGGGGGCCCCAGAGACACAAGCCCGAGGGTCTTCCCCC
GCCCCCTGCCAGATCACAGGAGACCAAGCAGCTGTGCTCCCGTG
CCTGAGAAATGCCCATCTGGGTACCAAAATCACCTCCAGAGGATAGA
GTGGGGGGCCAGGACAGGGGGACCCAGTTACAGAGCCCGAGGAGGCT
TCCAGGGGGGAGGGGACTCCGTTTGGGGCAGAGGGAGGAGAGGGG
CTGATGGATTCTCCCCGTTTCCGGATGCTGGCTGCTGGCTCCAGGA
GGCGGCGGTGCCATCTGATCTGATTAAGGCTGCACTCCAGCTGGGCG
GCACAGCTTGGGGGCTCGGCGGGCAGGGAAGAGGCGCTGTGCCCCAG
CGGTCAGGCTCGCTTCTCTTCTTCTCTCCATTAAAGTGTGAGAAC
CATTTATTGATTTTAAATCAGGACGTGCTGTCCGTGACACAGCAAGT
GAACAAAATCAGAGCAAGAGAGGGCCAGGGCTGAAGCCCGAGAGGGCGG
GCCTCAATCCGGGTGTGCCCCGGGGCTCCAGGCCCTTCTTCTTGG
GCTCTGGGCTAGTGGCCAGGCGAATGCACCTGCGCTCATCTGGGA
GGCTTGGCCATCGCTGGCTTCTGTCTCATGACGCACCGTCTTCCATATC
TACGGAACAGCTTCGCATTAAACAGGACAGGGAGGCGGTTGTTCTCTT
TATCTGCCACCATCGGCGCTGGGGCCAGTGGAGCCAGCGGGCTGACT
TCCCGCTCGCAGCAGGGCACTGATTGCAGGAACGAGGACATCCAGCCCC
CGCTCTCAATGCCCGGGTGTGAGAGCATTTCGCCAAACGGCTTGGG
TGGGACAAGGATGGAGCTGTGCGCCAGGGGCTGGCTGGGGCAGAAAGG
GGCTGCCCGTGTCTGCCGTGGCTCCAGCACCTCGGCTGCCAGGGTG
CTCTGGAGAGGTGCCCGGGGCGAGGGCCAGGGGCACCTGTTCTGCC
CACGTCTCTGTCTGTGAAAGTCCACAGACGCGTGTATACCTTG
GGAGTCAGGAGGATGGGGATAGTTGGGGCTTGACGTCTGTTCTGAAAA
AACACCGTTTCCCTGAAATATATATGTATTAAATTTTCTGCAAGATAAA
ACTGTGTATAGTTTCTGTGATGAGAAACGCATCCATCTTCTTAGAAA
GCCTGAAGAGGTACAGGAGCCTATAAAGGACAGATGACAGATGCCTTA
ACGCACACCAATGTGCGGTGGCCCCAGGGGACCGCATAGACGGGGCGG
CTCCAGATGGCCACCGTGTGCGAGGACACGGTTCAGGTTGCAGATAT

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FIGURE 6, CONTD.

TCCTGGGGGGGGGGCTCAGCGGTCCCATTTCCCCCTCCCTTCCTTCC
TTCATTTCTTCTTCTTCTTCTTCTTCTTGTGGTTTATGGGCGGCACCCG
CGGCGTGTGGAGGTTCCAGCCTAGGGGTCTAATCAGAGCTACAGCTGCC
GGCTCCACCACAGCTCAGGCAACGCCGATCCTTAACCCACGGAGCGA
GACCAGGGATGGAACCTGGGACCTCATGGATCTTAGTTGGGTTTGTTCCT
GCTGAGCCACAAACGGGAACCTCAGCCATTCCCATTTCTTGCTCAGTTCC
AAGAATTCCAATTCTTATTCCTGTTCTTTAAGGCCAGAGGCGACAGCCAC
GCCAGTCCAGAAAGCAGGGCTCAAGGATGCTGCTGTTGACTGTGTCCGT
GGCGGGGGGAGTTGATAAGAAACCCCAACACAGGGTGGTGGCCAGCAAC
GGGGAGGGAGGAGGGGGCTGGTGGCGAAAAGTCCCTGAACCCCATGG
GCTGCCCCCTCCAGGCTGGGGCAGACCCGAGCCCATGGCCGAGGAG
AAACGGTCCAGCCCCAGGCTGGGCTCCCGCACCCCTGCCCTGACCCCGC
Contig 115 (1895 bp)
TCATGGAAGCCCTTATCACAACCTCGGATCCAAAACCCACTGGCGAGTC
CAGGGATAGAATCGCATCCCCACAGACCTATGTTGGGGTCTTAACCAAG
CTGAGCCACATGGAACCTGGGTAATCTATTTTAGATGTTCTAGGGTTT
TTGGCCTTGCCGTGACGTGGGGACGCTGCTGGGCCAGGGATCAAAACCCG
GCCAGCTGTGACCAAGCAGAGCAGTGACAGCACCGGATCCTTAAGCA
CGAGCCAGCAGGAGCCCTGTGTTTAGATTGTTGAGGATACTGCGT
GGGATTCAGGATATTCATTTGGGGCTGTTGGAATTGCCCGTCCGTGTTT
AAGCAAGAGAAATCCCTTCACTCTGTGTAACGTGGGGGAATCCTTTAG
TCTCTTGAACCATTTGCGTGTGTTAAGAGTGGTAACCTGCCACCAATA
ATGCCAGACCAAGCCCTTCTGAGATCCGCTTTTGTGCAAAATATCTGG
TTTGAATGCTTTGATCGCCCGCACAGACAGGGTGGCGGACGCCGCCG
GGGACCCGACGTGACCATCGTGCTTCTGTATCCGCCCTTCTCCGGCAGC
CGCCCCCTGGTTGCCCTGCGCTGCTTTAGTGGAGGAATGAAGCCTCGC
CACCCAGACCCCGAGACCGCAGGACCCACAATGCTTCAAAACACCTGCCCT
CTGACTTTTACAGGTCAAGTTCCCAACGCCGAATTTGCACCGATTGGCT
ACAGAGAGCACGGTGGCGCAAGCCTCCACTTGGAGTTTATAAGGTCTC
CCTCCAGCTCGCAATGAAAATGAGCTGTGATAAGGCAAGACAAAATTAG
TATGAAATCCAGATGCTTCACTACAATACAATGACCCGGGATTGGGT
CTGAGCGACTGAAATCAAGGTGGGCTTCCGGAGGGAGGCTGTTAGAGGAA
AGGCATTACGGAGGCTCAGGTCCGAGAGGCTTCCACACCCCTAAGAGGG
CTGAGACGGCAAGTAGGACCAAGCCCCGAGTCGGGAGAGCTGGGCAGG
AAGGAAGTCTGAGGTACCCCCACCTGGGGAGGAAGTGCCTAGAGAAGCG
GGGGCGGGAAGCAGGGGATGCCAGTCCCAAGACAGGACAGGGCGGAAA
GGGCTCTCTGACGGCCCTCAATGCTGCCACAGTGTCTCGTAAGAGGGAG
GCAGAGAGAATTGACACCGGGGAGACCAAGGACCAAGGAGGTGGAGACC
GGGCTGCCCGCGGTGCCAGTTGCTCCCGAAGCCGCCCTCCCCAGAG
CCTTTGGGAAGAGGCCCAACCTGCAGTTCTGCTACTCGGGGACAGGGAC
AGGGACAGCCCCCTGGAGCCGCTCTTAGGGGCAGCATCCCCAGAACCT
TCCTTAACAGACCATCTGGAGAGAGATGGGTCTGGGCTGCAGCTCCTGGA
ACTGTTTTGCCACCCGGCGAGCAGCAGTGGGTGCCAGCCTGGGCTGCC
AGCCTCAGGGCCGGGAGGGCTGAGGGCACTGGGGCCCGGCTCTGGGACT
CCCCTGCTCCTGCCCGTGACAGACAGCCACCTCCAGCATCTGCTTCCT
GCCACCCACATCCCCAGGACCGTCAGCCAGGCATGCCCTGGCGTCGGC
CACTCACACCACAGGCCAGGAACCAAGGGGCAACACAGAAGGGCAGTT
GCCATCTGCAGATGGAATGGACAACTGGGGTCCGTGATGATGGCAGGCT
CTGGGCGCCCGGCTGGCAGGGAGCCAGGACTGTGCGGCCATCACAGGA
AGGGCATGACGGGGTGAAGCAAGAGTGGAAACCTTGCCACCCGCTGG
GCGCACATACCGGCCACCTGCAGCCCCACCCCATTTGTTTGCT

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SUBSTITUTE SHEET (RULE 26)

FIGURE 8

Contig 1 (1040 bp)

GCAGCGCCGGATCCTTAATTAACTGAGAGATCTGCGGCCGCGGCCAGGGTCTGCTTCTG
GCCAAGTGTGGGGCTCTGCTCCATCTGGCTCGGAGGTCCACCATGGCAAAGCTGGGG
TCCTCCCACTGAATATTGGGGGTCCACTCGTGCCAAAGGCTGGGTGTCCAGTGTGCCAA
CGGTACATGGAAGCAATGTCTTCCCAAGGACCGTCCAGGTGTGGTCAGGCTGGACAGC
TGTGAGTCCCTTCGGGACTAGACTTGGTGGCCGACCCTAGGGACCGTCCCGAGGGCCC
CCACGAGGCCAGGTGTTTGGCCCGAGGACAGAACGGCCAAGGGTGGCCGAGGGTCTTTT
TGTTTGTCTTTCTTCTTCTTCTTCTTCTTGGCCGAGGGTCTTAAAGCGCTCTCTCTG
CTCTTGTCCGATCCTGAGCGGGCAGTGTCTGCTGGTGGGTGCTGGCCAGCCGAG
CAGGGCTGAGAGAGCCCGCTTGTCACTAGGGCGCGCGGTGAGCCAGCGGCATGCCG
TGTCCAGACGTTGGATGGGGCAGCGAGGGGACTGGGTGCCAGCCCGCTGGGAAGCC
CGCCCTGTGGAAGCCGCTGTGCTCGCCACAACAAGCACCGTCCAGTGTGTGAATCAG
CGCCCGTTCGCGCGCTAATCCAGGCGCTTCTGCCCAACCTGAGCCCTGACCCACACC
CCTTGGCAGCCGCTCCGTGGACCTGGGGCGATGAGGTGAACCGTGGGCTGGCCATCGTG
GTGGCAGCGGTGGCACACCCGTGCGCTGTGCGCCCTCCATCCAGGAGCAGAGTGC
GCACCCAGTGGGGGCTGGGCAGGGAGCCGCTCCACCTCCGCCCTGAGGGGACGGGACTC
TTTCGACCCGAGGTGGGAAGGGACATATGCGGACGATGCCAGACCTGTCTGTGGGGGA
GGGGGAGAAGGCCCTCTTTGGAGAATTCCAGGACGGGTGAGGAACGTGTCTGGACCGGC
CGGTCGGAGGTGGGCCTTC

Contig 2 (9234 bp)

GGCAACCAGGGGAAGATGGGGAAGCGGGTGCAGCGGCTTTGCGCGGCCAAGGACCAC
CTTGGAAATCTGGAGCCTGGCAGGAGCGGGCAGGGTTGAGGGGCTGGCTTGGGCAGGGC
TGGCTGGCACCTGGGAGCCTGGCGGGTGTAGGTCGGGGCTCCAGGTCCCTATAGGCA
GGCCACATCCGCATGGGGGTGACAGGCCGAGCTGGGGTGGCGAGGGAAGAGGGGGA
GCCAGGCATTCAATCCCGCTCAATTTGGTTTCAGCTCGTCCCGCTGTGTCTAGGGGA
GTTGAGAGAGGTTCCGCCCGGGGCTGGGGCAGCGAGGTGTAGCTGGCAGCTGTGGGC
AGGTGAGGACAGCCGCTTGC CGGGCCAGGTGAGTCCCTTCCCTCCCGAGGCTTGTTC
TCTGGCTCTGCAATCCGAGGCTTCTGGGAGCGAGGGCCGGCGAGGCGAAGCGGCTGAC
CCCCGGCAGAGTGGCGCGGACACAGCCAAAGCGGGCAGAACAGGTGACACGTCTCAG
GGGGAGCTGGGACCGGGCGGGCTGGGGGCGGGGCGTCCAGGTGGAAAGACATCT
CAAGCGAGTCTGGTGGGAGACGAGGACGGGCTGCCAGGAGGAGACGCAACAGCGG
GGGGCATTCCAGGCCCGGGTGGACAGGACCCGTCGGGGTGTGAGGACAGTGGGGTCCC
CAGCGGCCACTTCACCCACTGCAATTATTAGTAGAGGTACAGGAGCGGCTCTGGCCG
GGCTCTTGAGGCTGAGCTGGAGCTCGAGGGCGGAGAATGGGAAGAGGTGCACTG
TGCCAGACAGAGCTCACCTGGAGGGAGCACGGCCGTGGGACGGGCCCCAGAGCAATTTC
GGCAGCAGGGAGGCTGGCGGGGCCAGGCTGGGAGCTGCGTTCCCAAGCAGACTGCGG
CCCAGGGGCTGGCGGGCAGGGCCCCGGTGTCTTGGTGGCACTGTGCGCCCTCGCGGC
TGGCCCTGGGACTGGCAGGGCAGACAGGACAGCACCGGGAGTCAAGGGCACTGACG
ACACCAGACTAGGCGAGGCGGGTGGGGTGGAAATGATGTGACCTCTGGGGGAGGGAGGT
GGGGACGAGGACAGGGGCGAGGCGCGGAGCTGGCGGCGAGCGAGGCCAAGGCGGGCT
CTGGCGGTGACAACTGAGCACATATGGGTACCTTTGGCTCGCACCGGAGACAGGTGAGT
GTCTGGCCCCGGCTTGGCGCCCTCCCGGCCCGCCACTGCTCTGCCCCCTCCCTCGACC
AGGGCCCTCTGCTTCCCCACAGCTCTGCTCCAGTGGGGTGGACACACTGCCAGCACC
CAGGCGGAGCGCAGGATGTGCTTGGAGGACATGACACAGTCCGGTCTACGGAGAGGG
ACAGAGCTGACGCGGTCCGGCTTCTGCTGAGGCGAGGTCCAGGCTTGGCCCCAGGC
CAGCGGCCCCACCCCGCCCTCATGGGCTCTTCTGTCCCGCAGAACACTCTCGGCTG
GCCCCGCGGGGAGCTGCCACACCCAGGCTGTGCTTGTCTTGTCTGCTGAAGGAGCAGT
GCATGACTGTGCTCTCTGGACCCAGAACCTCAACGACAAAGGTGAGGAGGTCCGCG
CTCGCCACACAGTGAAGGGGCGTGGCGAGAGCGGGCGCTACAGGTGCCCCCTCCC
CCTGCAGAGATGGTGTACCCAGCTCATGCTGGGCTTGGACCCGAGCTTCTTCAAGTC
CTCTAGTCTGACTCAAGAAATATGCTGCATTCTGGAGCCACTACACTACTTGACTCAGG

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[illegible]

-99-

FIGURE 8, CONTD.

AAGAGCAACGCTGAGCTAGCTCCACGCGTGGGTCCATCTCGGCCAGGTTTAAAGAGCC
ACTTTCAGGCAGGGATTGCACAGGAGGCAGGGTGGGAAGTGGCTCTGCTCAGACCCCTGA
ACAGGGCTCTGGAGATTCTCAAGGGCACAAAGAACGGACGATGCCCTGGGGTCAGCGA
CAATGCTCCCTGAGAAATCTTGGCACACAGGGCTGGGCTGGAGGTGGCCCTCGCCCC
ACCCAGCCTCTGGAGGACAAACGTCGCCCTGCTCCAGAGCTGGGGGGCCACACAGT
GGGGCACAGGGAGCATGGGCCGATTCCAGGCTGGGCTCCCTCTCGTCTCAGGATCTC
CCCGTCTTGTCTCAACAAGCCCTGACTTGGAGGCCCCAGGGTGACCCCTTAAAGGGG
GAACAGAAGGTTCTAGAAGGAGCGTGGCCAGCTTGGCTTCCCTAGGGCTGTGGTGACCA
CACTGGGCCACGGCCACGGCCACCCACCCGCTCTTCCCTTGGCCCTCCCTTCCC
CGCAGCTCTCCCTGGCTGCACCTGGTGACACGGCTGGCTCCAGCCAGGGCTGAGGGGG
ACCCAGGGGGCCCTTCTGGAAGCCACCTGCAGGCGGGCTTGTGGGAAGGGGCTGC
TCCTCGCCGGCCACCCGCGCCGGGCGCTTCTGGAAGCGGTCACTGGATATTTGTT
CCTTGTAGCGCCGAGCTTGCTATAAGCAGACACTGAGCTCCTTGTCTCCGGAGCAGC
CGCTCCATCACCAGAACCTTGGCCGACACAGGGCGGAGCCGGGCTGGGGAGCAGCG
CGGGCTGGGGCGGACCAAGCATACGGCGCCGAGCGCAGGGCCCGCCGCTTC
TGCAGGCCGCCCCACGTGCCAGGCCAGCGGTGCCATCTGCAGGCTGGGAGGAGGC
TGTGGGCGCAGAGCTGAGAAGGGGCGAGGCACTGGGGGGGACAGCCGTGTCCACA
CTTTGCAGAACTTGGCCGCTGGATGTCTTGTGGAGAGCTGGGGGAGGGGACAGG
CGAGGAAGCCGCTCCCGGAGCGGGTAGGAAGAGGCTCGGCCCTGGGAGGAGGAGGA
GGGAGGGCAGTGAGATGGAAGAGCACAGGGGCTCGAGGCTTCTTCTGGAACAAGGA
CTAGAAGGAGGAGGGCGGGAGCTGCTTGGGATGCTTGAACAGGCCCGCCAGTGCTG
ACAGGGACGTGACTGGGGCGCGTCCCGGCCAGGCGGGCTGGGAGGGCGCTGGTGG
GTACGGCCACTCAGAGCCCTGGCAGCAGGGGGCTGGGCAGGCTGCAGGACAGAGCTC
AGGACACAGATGGGGGCGAGGACTGAGTGGGGCACACAGATGCTCCAGGAGGTGGCCA
AGGAGTGGCTTGGGATCCAGGATGGCCCTGGTCCAGAAAGATGCGGCAGCCCAAGGGA
CCAGGCCAGGGCGCGAGGGGGCCACAATCTGAGCAGGGCTCAGGCCAGGGCAGAGGCC
CTCCACCCAGCCCTCCCTGGGCCGCTCTCC
GTGACGGCAGTGGGCTCAGATGGGGCAGACATGAGACCAGGTCCAGGGAGAAGCGGGCC
CCTTGGCTTCACTCAGGTGGCTTTCAGACCCGCGCCCTGCGTGGCAAGGCCACAGCGC
TCAGAGCACACAGACCCACACGGGCTCCCGAGGTGGGCGGTGACATCAGCCCTG
TGTCACAGCAGGAGCTGGCAGCTCCCGACCGGGCTTAGGGAGCGGGGACCTGAGCCA
CCTGCCACCCGCCACCCACCGTGGCCACACGAGGGCCCGCTGCTCTGGGTCTGGGG
CCAAGGCCCCCGAGGCGCTGGCAGTGTCTGCCCTCCCGTGGCTCTCCGTCCTCAGTG
TCCCGCCAGAGAGCATGGGGCCACAGGCTGAATGCCACCTCTTCTCTCTGAGAGG
GGGCTGAGGTTTGGGGTTACAGAGTGGCTCCGGGGTGGGTCCAGGCCACGCGAGG
CAAAGCGGACCCAGGAGTCCCGGGAATGTGGGACAGCCCGCTGAGATCTCGGGGG
GGCCAGCTCTGGTTGACCTCCATCTGGGGCTGTGGGCTTGGTCAGTGGGAGGGTC
ATGACACCCAGCCACAGCTGGTGACAGCCCTGGAGTGGCGGTCCAGGGCTGGCTTC
CCCTGCAGCTTGAACCCCTGTTCTCTGGGAGTGGGGCGCAGGGGGCGCGGGGAGGG
TGAGAGACGAGAGCTCTTCTCCAGAACTCTGCTGCGATGAGGACCCAGCAGGGGCC
TCTCTCACCAGAGGGCTCTGCCGGCTGCAGGGCCCGAGAGAGGCCAGAGGCTGGAGG
CGGGGCTTGGGAAGAGGCGGACTTCCAGAAACAGCTGCCCGCTCCGACACCCAGC
GCCACTTGGGAGGGGGCGCGCCCGTGGCCCGCCGGGTCCACTGCTGGGGCGGCCA
CAATAAGTTTGTCCCTGCTGGTTACTGTCCGTGTCTGAGAGGTTTCTGGAGCTGGCCA
CAATGGGCGTCAGGATGCGGCTGGGAGGAGCCCTCCGAGTCAGAGTGTGCTGGTCTCGG
ACAGGCCCGCGCGCCCGCCAGCCGTGCTCTGTGGACAGATGGTGGGTGGGTGGTGTCTG
GAGGGGTTGGAGAGGTTGGGCGGGACGAGGGGCTTCTGCACTGTCTCCAGGGAAGCG
GGGACCAAGGAGGGGACAGCCCGCTCACCAGGAGGTCCTGTCTCTCACCCTCCGCGG
GACAGGTGAGCTCCCGGAGCCGCTTCTGGGACAGGACCCAGGGCAGGCCAGGGCC
CCCCCACCCCGTGGTCCCTCCGTCCACGGCCGGCTGGGGGGCACGGGCCACGGGCC
CCCGCTCCCGCTTGGCCCTCCGAGGGTGAACGACCTCGCTGGGACGTGGGGCAGAGGGC
AGGCGCCAAGAGTGACCCCTGGGACAGCTGGCTGTTTGCAGTTCTGGAGGCAGCCGAGA
TAAAGCGGCTGTTTCCAGTGGGCTCAGGGCCAGAGGGGGCGAGGGGACGCCAGTC
AAGGCCGGGCGCTGCCCTGGGCTCCCTCTGTGCGGAGGAGGGGGCGGTTGCACAGC
AGCCCCCTGCCCGCCCGCCCGCCGCGCAGGACACGTGGGACCCGGCTGGTGGCCCCCT
CCCCCGCCCTGCTCAGGGGCCAGCCCTCTCTGGTCCCAGGACGCCCGCCCGCCGAGG
CGGCCAGAGAGTCCAGAGTGTAGCTTCCACGTGTGGGATCTGTATATGCGACAGC
TTAATCAGGCGCAATTTATGGGTCTGGATTGGGTGGGACAGGCCCTGCACAGCGG
GGCTGGAAGCCTAAGGCGGTGGGCTGGGGTGAGAGGCCCGCAGACACAGGAGGAGG
CTGGGACACTCAAGGGTTGACATGCTATGCTGTACGGATAAATGC

Contig 3 (5347 bp)

AGATGTGTATAAGAGACAGGGGCTGGGTGGGAAGGACAGAGGTGGGGCGGAGGAAATG

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FIGURE 8, CONTD.

GGATGCAGAGCCACCGTGACGCTCTGCTGGCCTTTAGCCTCGCTGAGTCGCAAGAAG
CCCTCGGGCCTGGAAACAGACCCCGGCCCCACCCCAACCCGCGCCCGGATTACCCC
GGCATGGCTGGAGGGCCCGAGAAGCCACCCAGGCTTCCCGTCCGAGCTGGGTGCTGGGC
CCAGCCGAGCGGGCTTGACGCCACGCTTAGCCCTCCCGAGGGAGCCAGGGTCGGAAGGA
AGAGGCCGCGGAGGGCCGTGGCCGCTCAGGCTGGAGGGGGCCCGGGTCAGGATGGG
CCCCAGAGCTCCCGCTCCCGGCCATCCGTCACGGAGCTGTACCCAGGAACGTGCTCC
AGACGTGCTTTCTGCGCGGAGGCCCGAGCAGGCTCCAGGCGCCCAACCCCGAAGC
CCACGCACACCTCGGTCTGCGAACACCTGCCGTATCCGGTGGCCCGGTTCCCGCC
GCCCGCGCATCCGGGTGCCCTTCTCCCTGGGTGGGGGCCATGCCCTCAGCGGGCAC
GCAGGCTGTGCAGGTCTGTCTGACTCTTCCCAAGACGACGGCCGGCTGCGGGCGCC
CCGACCTCGTCTAGGCCCGTTTGTGCTCACTGGCTGTCTCAGAAAGGGGTGCCACGGG
AAGCGGTGTTCTTGGGCGCAAGGCAAGGGAGGCCACCCCAAGGTGGCTGAGGGCAAA
TGGCCAGGGCTCTAAGGAGTCCCTGGGGCGGGCCGGCTGCAGCTTGAGGAGGAGA
GCCCTGGCTCTGCTCCCGGGCAGGTGAGCCACGGCAGGGGGCTCCCGAGAGCCTTG
GCAGGACGAGTGAGGAAGGGGTGAGGATGAAGGCAAGGGGGCTGCGGGGACTTGGGA
AAGCCCTGAAGAACTGAGTTCTCGGAAAGGCCGGAGCCCTCAGCCGAGCCTCGGCCCT
CAGCGATGAGGGCGGCCACCTGCGGCCCGAGGGTGAGCTGTGATCCGTCCCGCTCG
GGCTCCCGCTGCGCCCGCGGCCACCACTCTCCCGCTTTGCTTTGATCACTTGAGT
GCGACAGCTTGCGGGCTGAGCCAGAGACCGCTGCCCGCTGCCCGCAGCCCCACGG
GAGCGTCCACTTGGCGCTGGCCACTCATCCCTCCCGATGAGGCTTTCTAGCCT
GGCGCGCCCGGGAGCGCGACCCAGCCCTCGCCCGCTCCCGCAGTGAAGGTGCTGC
CTGGTGTCTGGGAAGCCCTGGAACAGGGGGCAGGTCCACACGGGTGCTCTGGCC
TCCAGCTGCCAGGGAGGGCGCGCTCAGGCCAGGGTCCCTCCACGAAACCCAGGGC
CTGGGGAACCTGTCTGTGTAACAGGGCCGCTCCCGGGACTCCACGGAGAGGTGGG
AGGGACCCCTGAGCACCCACCGCACTAAGGGGCCAGCCAGCTCGCGGGTGAGGCAGC
CGCTGGCGCTCATGCTACTGCTCTCTGGCTTTGTGTGTGCGCTGGGTGGGGTG
AGCGAGGTGCCGAAGCGGAAGAGCCACCTCCACTCGGGGACCTATTTCAGCAAGA
AGACGATGGGACTGCCGGCATGGACAAGGAACAGGATGAACCTTCTGGAACGACAA
GGCTCCACGGCTGACCGCTATAGGAAGCGCGCTCTAGGCCAATCCACCGTCCACCG
TCCATTCCCGAGCCTCGAGAGGGGGCAGGATGGACCGCTGCAGCGTGAGAGAGCTTG
GGCGTCCACAGGGCAAGTCCAGGGCACTGACCTCAGAGCCCAACAGGCCACCGGG
GCTGGGCCACAGGGAGCCGGGGCCAGGGTCAGGGTCAGGGCCAGAGTGCGGGAAAG
GTGGCGTGTGCTTGGGGCGCGGGCGCGACAGCGCCCTCGCACCCCGCAGAGCCCT
GGAGCTGAGTGAAGCCCGCGGGTACCTTGGCTGGGGTGGGGTCTCTGCGACCGCAC
CCAGCTCAGGTCTCTTGTGTACCGCAGAGGGGGCAGGGTCTGAGCAGGGACAGGG
TGGGCGCGCAGGAAGCCCTCTCTCTGAGGCTGCCCGGGCTGGAGCCTCTCTGGG
GCATGCCACCTCTCACAGACGCTCCAGGAGCCCACTTTCTGCTGCGTGGTGAG
GGTGTCTCTACCCGATTCCTGGCCCTGCAGGTGAGTGAGTCCCTGCTAAGCCTGGGG
TTGGAGCAGGTGACGGCATCACACACAGCAGCAGAGGCTGTGGGGCCCTGAGAGGC
GCTCCAGGTACCTCTCAGGGGGCTGAGCCCGGGGTGACCCGGGACCTCGCTGCC
CAAAGCCGGCGCCCTCTCCCGCCCGCCGACAGGGCCAGAGAAGCAGGTGTGGGGCGG
CACAAACCAAGTCAGCTTCCAGATCTGTCTGGGGCGCGT7GAAACTCGAAGCCCCAG
GCTGGGAGGTCTAGACACCCCTGCCAGACGACAGCCTGGGCTGGCTCACAGTGCCT
GGGGGCCAGGGGTGCACCTGCCCTGTGGGTGGGGTCCAGAGGGCAGGGAAACCTCGGA
AGGTCCCGAGGGTCAAGGTGGGGCTAAGCTCCGGTGACCTCTGGGAAGTCTGGGGCTG
GGTTTGTCTCCAGAGGAGAGAGGGCCAGTAGCCTCAGAGGGGTGTGGCAGGTGGGA
GGCCCCAGGTGACCCAGAGCGTGCAGAGCAAGCCCTTGACTGCAAGC
GCAAGGGCAGAGGTGGGGTGGGAGCTCGACCCCGAGCCAGGTACACAGGGGGAAG
GGCGAGGGATCCGGCAGGGGCCACACCCGCCACCCAGGCAGCCCAAAAGCCTTGGGC
CCGGAGCCAGATGGGCCAGCCAGCTCTGGGAACAGTCTCCAGAAATCCCGAGCT
CTGGGTACCAACAGGGCTGCCCGGGCCCGAGGCCCTCGGGCGGGAGACCTTCCCGAGG
GGATCTCTAAGTGGCAAGGCCGTGTGGGAGGGGTGGTGAGAGGCCACTTGGCGGGA
AGACCCCGACCCCTGGAGCCCTAGCCACTGCTGCTGCGGCTCCCTAGGGATCCAGG
GCCATCAGAGAAGCTCCAGCGCACTGTTATTTTCAAATGACACTTTTAAAGAAAAACA
GCCTCACCAAAATGCTTGGCCCTGAGTCTGGAATGTGCAGACAGACAGCTGCCCCCTCC
AGAGCTGCACGGCCCTCCGGGTGGGGAGGAGCAGGGGGCACCCCTGGGACCGGGCCGC
AGGCTGTAGGGCACGGAACGTGTCTTGGGCCCTGTCTCAATTCCCGGTGCCAGTGG
CCCCAATCTCCAGCAGACCCAGAGGGGCCAGCTTGTCTTGGCTGGCCGTGGTCTCT
GTCACCCAGGCTGGAGTTCTGGAAGATTCTGCTCTGCTCCCGTGTGCACATACCACT
CCCCGGGGCAGCCCTGCACCTTGTCTTCTGCTGGGCTCCCTGCTGATCCGTGAGGCT
GCAGCCCGCTGATCTCCAGGTCTCTCCGAGCCCGCGCTCCAGGAAGCCCTCCAGG
AGAGCTCAGGAGGGTGGGCTCCCTGCGCGCAGCTGTGACACCCCTGGGGCCAGCCCGCG
GCTGTAGGGTCCAGGT7TCCCAAGCCCTCGGGCAGAGGCTGGGGCGCTGGGTCCCTC
GGAGCAACTGGCTCCGAGGCCCTTCCCTAGACGGGT7TCCGGGAGCCCTCCCGAGCGG

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FIGURE 8, CONTD.

CACCCACTGAGTTTTGAACACTTGGCGCCACCCACACCCAGGCGGTGGCCAGGAGGC
CTCCTGGGCAGCAGACAGTCCGTGAGGTGGCCCTGGGGTGGCTCCTGACCTGGGCGCTGG
CCCAGCCCTGGGCACAGCTTCCAGATCTTGCTGCGGCTTCTCCAGGCTGCCTCGGCC
CCTCCCGCTGGGGTGGCCAGCTTTCTGAGGATGCCACCTTGCCATGGTCAGG
GAGGGGCTGAGAAACCCACCTCGTGCTCTGCCCGGCTATGCCAGGGGAACAGGTTT
CCTCCCGCAGGAGGGGACCGAGTCCCTGACAGCCCACTGCAGAGGGAGGAGTGCCTGG
CTCTGCCCCAGCCCCACCAACCCCGTGGCTTCTGTTCGACGCCCAAGCACTAAA
GGCCGAGGTCTTGAACATCAAGACCCGGGAAGTCCATTGTATTGAATTGAGTGA
TGAGCCTGAGGCTGTGGCTTGCCTTTCCACAATTACCGCTGCCCGGAAGGGCTCCGG
AACCGACACAGCCCCAGGGCCCCCTGCCATGTGGGAGCCAGGCTGGCTGAAGAAG
CCCCATAAGGTGGACCCCACTTTGAGCCCCACAGAGTGGGCCAAGGACAGGTGAGG
GCTGCCAGGCTCTGGGCTCTCTGCTGCCAGGTGGGCTCCTCGGGGCCAGGCTGG
CCTGCGGAGCTTCCACGCTGAGTTCCCGAGCTGGTATGAGCGTAGTGGACCGCAGCC
ATGCCAGCACTCAGGGGCTGAGGGACAGAGCGGGAATCCAGCCCCGGGTCTCGGC
CCCTAGGATCTCTAGGTGGGGAAGCCCAAGGAGCAGAGGGGTGAACGCAAGCTGTGTG
GGGCCCCAGGCTGCCAGCAGACCCCTCTGCTCCACTCTCGGCGAGTGGGCGCCGAG
ATGCCGGGGCAGTGCCATTTCCAGGCGCCACCGGAGGCTCCAGAGGGAGTGAAGCAGG
AGCTGGGAGGGAGGGCGGGGGGCTGGGAGGCAAGAGCGGAGGCCGAGGCGGCTGAG
GAGGCCCGGAGGGGCTGGAGTCAATGACCCAGGGATTATCGTGTGGGTCTTTGCAAA
GTTGGCTGAGCAACGCCGGAGCCAGGGTCAAGGAGACGGGACTGGCGGGCCCCCGGG
CCCCCTTTCCCTTTCTGGAAGAAAGCTGTTCCAGGTCAAAATCCAGCTCATGATCCG
CCCCCTTTGGGACTGATGTTGAGAGGCCAGTGGTCCAGCACCTCTGTCACCGCCCC
CCACGCTCCCGGGCGGCCAACCCCTGTGGGCTGCGAGGTGCGGGCACCTCTCCCTTCG
AAGCAAGCCCTGCCCTGCGTGGGCGAGCTGATTCTCTCTCTGGGCTGCACCTTG
ACTGGGTGGGGGGTGG

Contig 4 (1592 bp)

AGCCCCCAGCCCCCTCCGAGCAGCTGCTGGGCTCAGCGGCTCGCCCCCGATGTGCGGC
CCTCCATAATCAATCATGAGGGGCGGGCCCGGGGGGGCGGGCCGACCTGTACGCCAGC
TCCAAGGGCAGGGACAGCTGCTGTTCCGGAGGGTTCCAGGGGCCAGCCCCACAGACAG
CGGCCTCGGCCCCCTTCCCGAGGGGACCCCCACGGAGGGCCAGACCGGAGGACTC
GGGGCCAGAGGGCAGGGCAAGAGTGAAGGACAGCGCGGTGGGAGCGCGGTGAGCGGG
TCCAGGGCTTCAATTCCCAAGGAGCCCATGCCCTGAGCCGCACTGAGCCCTGTGACGCC
TGTGGGTGCGCGCAGGGCCGCCACCCCGCCCCACAGGCTGGGGTCAAGAGGAGGAG
GGGTGGCTGACGGAATGGTAACAGCTGCTCCCCCACCTCGCCGGCTGGACAGGGCTC
GCTTCTCTGCCCCAGCCCCCGGTGCCCATCCGTACGGGCCACCCAGGACTGTGCGT
CCAGCCTCCCTCCCTCAATCCCCCGCATTTCCGAATTCTCGGGCCACTGTGCTTC
CTCTCAAAATTCCTGGCCCCCTCGCCCCATCCCGCCATGGGAAAGGGCCGCGATGCCA
GGACACTTGCTCGTCTCGGCCGGGGGGGGGAGGAGCAGCTGGCTGGGCGCGGAGCTGT
GAGGTGCGGGGGTGCAGGGAGAAGGGCCAGATTAGGGGGCGTATGGGAAAGCTGGGA
GGGAACGCTACCCAGAGCCCTCCTGCCGAGCCTGTGCTGCTCCTCTCCGCAATTCTG
GCCTCTGAGTGCTCCCTGGAGGGAAGGGACCACTGTGCTCTGCCGGCTCTGGCTCTGCC
AGGAATGTCCATCTGTCCGGGCGGGTTACCTGGCTCAGAGCGTGGTACCAGCTCATCC
AGCCCTGACGCTGCTCTCGGGAACAGTGGATGGGCCAGGCGCCCCCGTACACCCCGCA
GCTGGGCTCCACAGACGGGCCCGGGATGGCCACGGAGGTGGGGGGCGGCCAGGGCGAG
GCTCCCTCTTGAAGGGCTAGAGTGTGGGCTGCGCGGAGAGGGAGGGCGGACGCCAGGC
CAGGTGCAGCCCCGGGCAAGTGTGTTGGGGCTGTGACCCACGCTGTGAGCTCAAGGGT
CCAGGAGCCCCAGGGACAGAGCCTCAGGGACAGACCTCAGAGCCACAGCAGGAAGCCTG
GTGGCAGTAGCTGGCGGGGCCGTGGGGTGTCTCGGCCCTGCAGACAGAGGACAGGACGGC
TCCCTGCTGATGACAGGGGCTTTCTCTGTCCCTGGGGGGCGGAGGGGGCCGACCATGG
ACCCCGGGCTCTCTGCGACGATTCCAGGGCCAGCTGGTCTCAGGCAGTCCAGGTTG
CACAATGGTCTCCATCGTCCAGAGTTGACAGCCAGCACTCTCCACTGGACGGCGGCC
GGGGTGGGCTGACCCGCCGCTCAGGGCTCAGGGCGCGGGCGGCCAGCCNCCGACGGCC
TTGACCTGTCTTATACACATCTCAACCTG

Contig 5 (831 bp)

TGAGATGTGTATAAGAGACAGGCCTTGACCTGGGCTGGCTCAGCTGCGCGCCCTCCTC
CTTGACAGCTCCGCTCGACCCCATCCATCAGCCATTTTCTACCTTCTGTATAAAAA
ACCCGAAGCGCGTGGCCCGTGTCCGTGGGGTGAATCGGCTGCTGTGTGGTGGCTC
CCACCTGGGCGCGGCCCTGAAACACACACCCGGGATGGCTTGCCCGGGGCTGGT
GGAGGGGGCGGGGGCTCGCTGCTCTGTCTGAAATTTTCGGTCCCATGCCCCGAC
TCCTCTCCGGCCACCTGCAAGGCCGGCGGTGCCCCGCCACTTTCCGAAGGACGG

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FIGURE 8, CONTD.

ACTCAGCATTTCAGGGGCACCTGCTGATGGTGCCAGACCCGGGGGCTTCCCGCCGG
GCGCGGCCACAGTCGCCCCCTCAGTGGCCACAGCGGGCTGGGCCAAGGCTGGGAGTTC
TGACAGGGCTGGGGAGGAAGCGGGGAGAGGGGACAGTCTCTGGCGGGGACGAGGG
TGGGGGACAGAGTGGGGAGTTCCACAGCCGGGGACGGGGACGCGCTTGGCTGCCCT
GGGTCTCAGCGGGGACAGTGCCACAGGAGAGAGCGGCAGACAGTACAGCCACCCG
TTTTATATCTCTCAGGCGGTCTGTGCTTTATGGGGTAAATATGCAGGACATAGAACT
CTGCCACTGGACCCCTTGGCGGGGGACAGCAGCGGCATTGCTGCTTCTGGGTGCA
GCGACCCAGCACACCGGGCAGAGCACCCTATCTTCCGATCAACCGGAC

Contig 6 (4634 bp)

CTCTGGGCTAGCACCGTGGGGGCTTGGCCAGAGTGGAACTGAACTGGGTCCACCCGGAG
CCAGAGGGCGGTGAATGGGAGGCAGAGCCATCTCGGAATGGACCAGAAGAGGGAG
CGGGGGTGGGGAGGGGGCATCAGATCTGGTCTTCTTGTGCGCTGCGGTCCCTTGC
CACCCTCCCCGAAGCTGATCTGGAGCACAGCGCTCGTTAAAGCCGCATCAGAGCCCA
CTTCTGACAGACGGAAGGGGCGAGTGCCTTCTCACCAGGCTCGCCCTGGGAAGGGCC
CTCCCTGCAGCCAGGAAGCCAGCAGAGGTGACAGAGCCAGGGGCCAGGGCCCCAGGG
ACGGGCTCGCGCGCCGAGCCGGGGTCCCTTGGCGTCCCATCTCTCGTCTGGAGCC
CTCTGGGTGACCACAGGAATGTGAAGCGGCAGCGGGTGGCGCGGGAGGCGGGTG
GGAGCGGGCGGGGTGGCTCTTACGGCGGGCTGAGAGATGGGCGCCGCTCGGGCC
TGGCGTATCGTCTCGCGCTCTTACCACTGAGCAAGACACAGAAATGAAGCTCGAA
CGAGCACAGCCAAAGACGGCCGTTCTGTCTTCTTCTTAACTCCCTTGGCTTAGGGT
TTCCCGGCTGGACAGCTGCCCCAAGGGCACATGGGCATCCGTCCGGGGACATTAGGCA
GTACCAATCCAGGCCACCCAGGCTGTGCCCTGCGTCTGGGCGATTTCAGCGCGGCC
AGAGATGGAGCAGCCACTGCGGGTCCCCGAGTCTCGGTGAGACAGTCAAGGATGGACCT
GGATGGAGACCGCGTGGCCATGTCCCTGGGTGAAGAGGCGTGCAGGCGGTGCTGGG
GGACATGGTGTCTGCCCTCGGCCAAACCATGAAAGAGCGCTCTCCCCAACCCCA
GCACCAACCCGAGACACCTCGGCGGAGCCAGCACGCCACCGTCAAGTCTCGGT
GTCCAGCTTGGGACAGGTGAGTCCAGATGTCCAGGCTGGAGCTGGTCTTGAAGATCC
TAGGGGTCCAGCCAGCACAGGAGGGCCAGGTGAGAGCCCTGTGGTCTTAAGGATGCA
ACCAGGGCGGGCGGGTGCCTGCCCTAGAGGGGTAACCTCGGCCCTGGGGACAGTC
ACCCAGAGGTCCCCAGAGCCAGCTCGGAGGGCCACAGGTGCCAGAGTCCACCTGG
GGAAGGCTGCCCTCTGCCAGCCCCGAGCGGGCCCTGGCGCCGCGTCCAGCCCG
ACCCCGGGGAGATATTACCCCTGCCCCGTGAATCAGGAGGCCCGAGGCCATGTTT
CAGTCTTTTCTCCATCCAGCCCCCAGGAGAAGAGGTGCTGAAGTGGGTCCCTGG
AGGCTCTGAGCCCCAGAACAGTGCCTCTGAGCAGACGGGCACTCTCAGACAGCTCAC
GCTGGACAAGTCACTCTGCTGCCGCTGATGGGCTTGGGAGAAGCAGACATGGTG
AGGAAAGGCCCTGTGCCCTTACCTAATTCGCCAGCCCAAGTCCCACTGGGTGCC
AGCTTCAACCTAAGCAATAATTCGTGCCCTTAAACAAACGCGGGGAATCCACCTGC
CTTCCCCGCCCCCCCC
ACCCCTGGCTTGACCTCCAAAAGCACTTGAAGGGGCTTCTCCAGACACCTCCAACCC
CGACCCCATGAAGAAGGGGTGATGGGCTGTTACCCCAACAAGCAAGAGAAGCAAGCCCA
GAGAGGAGTTGGCGTGGACAGCAGGGGTGAGGCCCTTGGCCCGAGGGCAGGGCTGGTG
CCACCTGGGTGAGCGGCAGGCCCTGGAAGAAGCAGCGGAATGAGCACACTGGGTCTCT
AGAAGGTTCTCCAGACCTCTGGGGCTGAGTCAATTCACACTCTGGGCGGGCAGGG
CTTCTTCTGGGCCCGAGGGGACAAGTCCCTTCTGTCGGGGGTACGGCCCTGGACCC
CTGTCCCCCGCACCCACCTCCGCTGGTGAGGGCGCGGCCAGCTCTGGACACAGATC
CCTCAGAGCCCTTCTCCCTCCCTGCTCCTCGTCTTCCCAAGATGCCCCGGCTCCAGG
TGGGGCAGCCAGGCGGCAGAAATGTGGTCCAGGCTCTCGGCCCAACCCACACCCCTGC
TCTGCCCTGACAGCTCTCAAGACGAGGACGCTGCTGGTCTGCGTCTGTCTCTCTCA
TGGCACAAACGGTGGCGCTAGCTTCCCAAGAGAAGGAGATCGTCTCCCGGACG
GACCTGCTGCTGTCTCTCCGCGGCTTACGGGCTCTCCCAAGGGTGGCGCG
AGGAGGCTCTGCTCCGGCCAGGGGCTCCATCTCCGAGCCGACAGGCTCCGCG
TGGTGGTCCGACCTTCTCCCAAGGCGCGCCATCTCTCGCGCTCCCCAAACCTG
CCTCTTCCCCAGCGCCCTGTCCCCAGGAAGACCTCCACCCGTGCCATTACAGCTC
TCGCCCCACCTCCAGCCACCCCTTCCCATCTCTCTGGAAGCTCCACTTCTTC
CGTCTCCACGGCAGCAGAGGCTCAGAGCTCAGGGTCTTGGGGCTGGAGATGGCC
TGCCCGGGGTCTGCTGACCGCTCTACGGAAGCTGTGCCGGGGGTGGGGTGTCTC
TGCCCAAGGGCTGGAGGACGAGCCATCCAGGGCAGCGGAACCTGCGTCTGGTCT
GAGACGGAGAGGCTGGGTGAGGTGGTGGGGGCTGCACACAGCTTGGCTGGGGTCC
CTAGGTGACAACTGGCTGAACACTATTGCTGCTCCCTTCCAGGGTGACCTGGGG
TCCCGTGTGGCCCTCAGGGCACAGGGGGCCCAAGGCTCACAGAACCCAGTGGG
ACTGCACCCAGGCCACAGAGTGGGGGCACTGGGGTCCAGAAACACCCCAAC

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FIGURE 8, CONTD.

CAGGCCAAGGTGGCCAAGGCCTTACTCGAGCGGGGCTGCCGTCCCAAGAGACTCTGGCC
AGTCGTCCGGATCCAGCTTCCCGGGCCGGGCCCGCTGGGCTCCAGGCGGTCTGGG
GGGCCCTCCCCGGGGTTCGCCCTCCGCTCTCAGCAGCAGGAAGAGGAGCGCGCCAGC
GGATGGGGAGAAGAGGGCGCCCTGGCCATCTTCTCCCCCTGGGACTTGAGGAGGGTCTC
GGGCCGGGCAGGCGGGACCGGGAGCCACAGAGACCCTGGAGGAGGCAGCATGGCGGGAG
GTGACCGGGGAAGAGGGCCGTGTCCAGGGCTCAGAGCCCGGCTGGCCCGCGCCCTCG
GGAGCGTGGCCGTGACCGCTGGCCGGGAGGTTTGTGCGGTGGGGTTTGAGAAAGT
GCTGAGCTGCTGAGCCACAGGCCAGGCTCAGAGGGGACAGGAAGGAGGTTGCTGCCAG
CCTCGGGCACTGCTGACCATCTCCCGTTTCCAGGGCACCAGAGCCACCTAATCTGCCGG
CTCTGTGCCAGGGACAGGCTTGCTGATCTCTCAAGGCCGGGCGCTCCGCTTCCCTGG
GAGAGGGTTAAACATCCAGCCCCAGCCAGCATCTCGGGCAGGTTCTTGCTCCCCCGCT
CGTGCTCTCTGAGACCTGTGTCGGCACACTTTCCTTGAGAGGAGGAGGAGGAGGAA
AGCGGATGGAACAGTGACCTGCGAGCCCTGAGGGACCTTCCACGTGCCCGCGCCG
CCCCCGCTCTCCGCCCCAGTCTCAGGCCCCAGTCTGATGGAGGGAGGGCGACCTC
CGGGCTCCCTGGCTCCCGCGGCTCCGGAAGACAGGGCCGCTCGGCTGGGGCTGAGGGA
GGGGCCCGAGAGCGAGGAGAGCAGCCGAGGCAACCCCGCGGCTCTCCAGAAGGAGG
CCTGGCAGGGGAGGGGGTGCCACCACTGCTGTCTCTCGTGCCACAGTGAGGGTGT
GGGTGGGCACTGCCGGGTGGGAAGTGAGAAAGACCCTGGACCGTGGGGCTGGGCCGCC
ACGGGGGAGCGGGTCTGTACGGGACCTGGGGGAGGAGGCGAAGGGCTGGGGCAGAGG
CCGGATCACTTCCAGATTGCTGTGGGACCAAGGGCCGACCTCGGGTGACTTCTTTTG
TGTGCTGGCCACAGGGGGCCCCGGCAGGTCACACGGAAGGGGCTTCGACCTGGCCT
AACAAAGCCACTCCGAGGAAGATGCAAGGGGAGGCAGACGGAAGGGCCGAAGGGGGCA
TCGGGGGACACCGGGCAGGGCCGGGGCAGAGAAGGGAGGCAGAGGGCAGAGAAGGGAGG
CAGAGGGCAGAGAAGGGAGGCAGAGGGCCACATGCTTGGAGGGCCAGGGAGGAGCGGGA
ACGGCTCCGGCTCCAGCGCCGAATCAGGCCCGTCAGGCGGAGGGTGCCTGGACCTGCC
TGGCCTTACGAGCACAGTCAGCAGGCTGTCTCTTATACACATCTCAACCATCAT

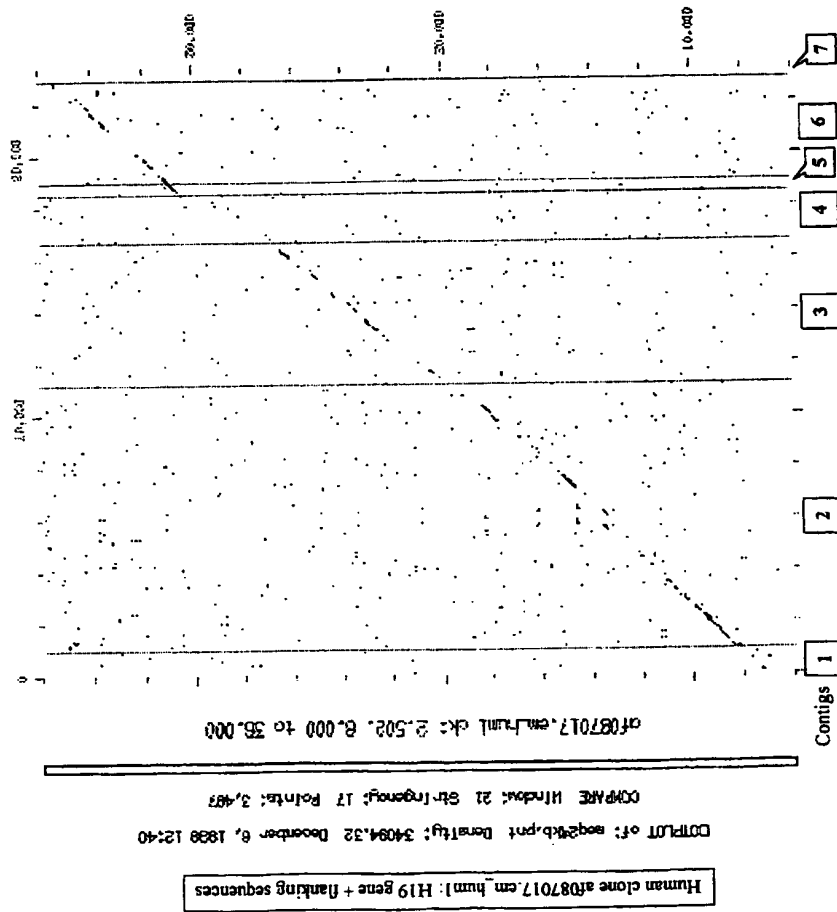
Contig 7 (482 bp)

AGCAATGGGGCCGTGACCTAAGGAGGCAGGCCAGGTCAGTGGGGTGACCTCTCGTGGCC
CCGATGTTTGAAATCCCCAAATCAAAATGACCCATCCGACAAGCTTGCATGCCGTCAGG
TCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGCCCTATAGTGAGTCTGATTAC
AATTCACCTGGCCGTGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACTT
AATCGCCTTGACGACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACC
GATCGCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTT
CTCCTTACGCATCTGTGCGGTATTTACACCCGATATGGTGCACTCTCAGTACAATCTGC
TCTGATGCCGATAGTTAAGCCAGCCCCGACACCCGCCAACCCGCTGACGCGAACCC
TT

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FIGURE 9

Human clone af087017.em_hum1: H19 gene + flanking sequences



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FIGURE 10

IDENTIFIED POLYMORPHISMS:POLYMORPHISMS TYROSINE HYDROXYLASE GENE - CONTIG C3 (figure 6)

1	GGATCCAGCC (A:T) GCAGCC	1081 bp
2	ACAACCCCC (-:C) TCCCACAG	1149 bp
3	TGCGGAGGGG (A:G) GACCTG	1186 bp
4	AGGT (CAAGGCCAGGT: -) CGAGG	1210 bp

POLYMORPHISMS INSULIN-IGF2 - CONTIG C4 (figure 6)

5	CCC (C:A) CCCC (A:C) CGCCGC	438 bp
6	CCC (C:A) CCCC (A:C) CGCCGC	443 bp
7	CGCCGCAGCA (G:A) GCCG	455 bp
8	GCTTATGG (G:A) GCCGGG	503 bp
9	CACGGC (T:C) TC (G:A) GAGCA	525 bp
10	CACGGC (T:C) TC (G:A) GAGCA	528 bp
11	GTCTGC (A:G) GGCAGGTG	571 bp
12	CAAGCCCGG (G:T) CGGTT	636 bp
13	ACCTC (A:G) AGGCCCCCA	710 bp
14	GC (C:T) GGGCCCAGCCGC	867 bp
15	ACCAGCTG (C:T) GTTCCC	903 bp
16	GGC (C:G) CTCTGGGCGCC	1148 bp
17	GGGGG (C:T) GTCCCGGA	1305 bp

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FIGURE 10, CONTD.

18	GCGGT (C:T) GGGGGAGTT	1320 bp
19	CGCCC (C:T) GTCCCGCT	1400 bp
20	TCCC (G:A) TCTCCGGCC	1519 bp
21	GA (T:A) GCCCCATCCCCC	1547 bp
22	GG (C:T) GGCTGCTGCGGC	1607 bp
23	TGGCTGC (G:A) GTCTGGG	2222 bp

POLYMORPHISMS IN CODING REGION - CONTIG C10 (figure 6)

24	GCGCA (G:T) TGATTGGCA	341 bp
25	CGCCCCCCCC (-:C) (G:C) GG	2247 bp
26	CGCCCCCCCC (-:C) (G:C) GG	2248 bp
27	GCAGCCGGCTC (C:T) TGG	2257 bp
28	GTTGTG (C:T) TCTGGGA	2413 bp

MICROSATELLITES

29	PIGQTL1: (AT) ¹¹	112 to 133 bp Contig 57
30	PIGQTL2: (GT) ⁸ GCACGCTGTGGCTGTGTAC (GT) ¹⁷	1074 to 1144 bp Contig 95
31	PIGQTL3: (CA) ¹⁹	223 to 260 bp Contig 105

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